WEST Search History

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DATE: Tuesday, January 02, 2007

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT; PLUR=YES; OP=OR	
☐	L27	reporter.clm. and l26	7
☐	L26	DNA and l24	8
☐	L25	L21	234
☐	L24	Joung-J$.in.	67
		DB=USPT; PLUR=YES; OP=OR	
☐	L23	L21	75
		DB=PGPB,USPT; PLUR=YES; OP=OR	
☐	L22	identif$ with(DNA adj binding adj protein) same (bind$ or interact$) same DNA with domain same reporter same fusion	5
☐	L21	identif$ with(DNA adj binding adj protein) same (bind$ or interact$) same DNA with domain	234
☐	L20	identif$ with(DNA adj binding adj protein) same (bind$ or interact$) same DNA with domain and l8	14
☐	L19	(reporter with gene) same identif$ with(DNA with binding with protein) same (bind$ or interact$) same domain and l8	32
		DB=USPT; PLUR=YES; OP=OR	
☐	L18	L17	137
		DB=PGPB,USPT; PLUR=YES; OP=OR	
☐	L17	(reporter with gene) same (DNA with binding with protein) same (bind$ or interact$) same domain and l8	391
☐	L16	(second adj reporter with gene) same (DNA with binding with protein) same (bind$ or interact$) same domain and l8	8
☐	L15	(DNA with binding with protein) same (bind$ or interact$) same domain and l8	411
☐	L14	(DNA with binding with domain) same interact$ same (test adj (peptide or polypeptide)) and l8	54
☐	L13	DNA with interact$ with (peptide or polypeptide) and l8	172
☐	L12	(second adj reporter with gene) same (DNA adj bind$ adj domain with fusion with (peptide or $peptide))	8
☐	L11	((first and second) adj reporter with gene) same (DNA adj bind$ adj domain with fusion with (peptide or $peptide))	8
☐	L10	((first and second) with reporter with gene) same (DNA with bind$ with domain with fusion with (peptide or $peptide))	83
☐	L9	(reporter with gene) same (DNA with bind$ with domain with fusion with	399

		(peptide or $peptide))	
☐	L8	(reporter with gene) same (DNA with bind$ with fusion with (peptide or $peptide))	437
☐	L7	(second with reporter with gene) same (DNA with bind$) same fusion	405
☐	L6	(reporter with gene) same (DNA with bind$) same fusion	2384
☐	L5	20030003449.pn.	1
☐	L4	(second with reporter) and L1	1
☐	L3	(activation with domain) and L1	1
☐	L2	(activation with tag) and L1	1
☐	L1	10/915233	1

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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2		"Ask CAS" for self-help around the clock
NEWS 3	AUG 09	INSPEC enhanced with 1898-1968 archive
NEWS 4	AUG 28	ADISCTI Reloaded and Enhanced
NEWS 5	AUG 30	CA(SM)/CAplus(SM) Austrian patent law changes
NEWS 6	SEP 21	CA/CAplus fields enhanced with simultaneous left and right truncation
NEWS 7	SEP 25	CA(SM)/CAplus(SM) display of CA Lexicon enhanced
NEWS 8	SEP 25	CAS REGISTRY(SM) no longer includes Concord 3D coordinates
NEWS 9	SEP 25	CAS REGISTRY(SM) updated with amino acid codes for pyrrolysine
NEWS 10	SEP 28	CEABA-VTB classification code fields reloaded with new classification scheme
NEWS 11	OCT 19	LOGOFF HOLD duration extended to 120 minutes
NEWS 12	OCT 19	E-mail format enhanced
NEWS 13	OCT 23	Option to turn off MARPAT highlighting enhancements available
NEWS 14	OCT 23	CAS Registry Number crossover limit increased to 300,000 in multiple databases
NEWS 15	OCT 23	The Derwent World Patents Index suite of databases on STN has been enhanced and reloaded
NEWS 16	OCT 30	CHEMLIST enhanced with new search and display field
NEWS 17	NOV 03	JAPIO enhanced with IPC 8 features and functionality
NEWS 18	NOV 10	CA/CAplus F-Term thesaurus enhanced
NEWS 19	NOV 10	STN Express with Discover! free maintenance release Version 8.01c now available
NEWS 20	NOV 20	CAS Registry Number crossover limit increased to 300,000 in additional databases
NEWS 21	NOV 20	CA/CAplus to MARPAT accession number crossover limit increased to 50,000
NEWS 22	DEC 01	CAS REGISTRY updated with new ambiguity codes
NEWS 23	DEC 11	CAS REGISTRY chemical nomenclature enhanced
NEWS 24	DEC 14	WPIDS/WPINDEX/WPIX manual codes updated
NEWS 25	DEC 14	GBFULL and FRFULL enhanced with IPC 8 features and functionality
NEWS 26	DEC 18	CA/CAplus pre-1967 chemical substance index entries enhanced with preparation role
NEWS 27	DEC 18	CA/CAplus patent kind codes updated
NEWS 28	DEC 18	MARPAT to CA/CAplus accession number crossover limit increased to 50,000
NEWS 29	DEC 18	MEDLINE updated in preparation for 2007 reload
NEWS 30	DEC 27	CA/CAplus enhanced with more pre-1907 records

NEWS EXPRESS NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.

NEWS HOURS STN Operating Hours Plus Help Desk Availability

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 NEWS IPC8      For general information regarding STN implementation of IPC 8
 NEWS X25       X.25 communication option no longer available

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FILE 'HOME' ENTERED AT 14:35:08 ON 02 JAN 2007

=> fil medline biosis caplus scisearch embase wpids
COST IN U.S. DOLLARS                                  SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.21       0.21

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=> identif (s) (DNA adj binding adj protein) and (bind or interact) (s) DNA (s)
domain and reporter and fusion
UNMATCHED RIGHT PARENTHESIS ') '
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> identif? (s) (DNA adj binding adj protein) and (bind or interact) (s) DNA (s)
domain and reporter and fusion
L1             0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN) AND (BIND OR INTERACT
                 ) (S) DNA (S) DOMAIN AND REPORTER AND FUSION

=> identif? (s) (DNA adj binding adj protein) and (bind or interact) (s) DNA (s)
domain and reporter
L2             0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN) AND (BIND OR INTERACT
                 ) (S) DNA (S) DOMAIN AND REPORTER

=> identif? (s) (DNA adj binding adj protein) and (bind or interact) (s) DNA (s)
domain and fusion
L3             0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN) AND (BIND OR INTERACT
                 ) (S) DNA (S) DOMAIN AND FUSION
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=> identif? (s) (DNA adj binding adj protein) and (bind or interact) (s) DNA (s)
domain
L4            0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN) AND (BIND OR INTERACT
                ) (S) DNA (S) DOMAIN

=> identif? (s) (DNA adj binding adj protein)
L5            0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN)

=> identif (s) (DNA (w) binding (w)  protein) and (bind or interact) (s) DNA (s)
domain and reporter and fusion
L6            0 IDENTIF (S) (DNA (W) BINDING (W) PROTEIN) AND (BIND OR INTERACT)
                (S) DNA (S) DOMAIN AND REPORTER AND FUSION

=> identif (s) (DNA (a) binding (a)  protein) and (bind or interact) (s) DNA (s)
domain and reporter and fusion
L7            0 IDENTIF (S) (DNA (A) BINDING (A) PROTEIN) AND (BIND OR INTERACT)
                (S) DNA (S) DOMAIN AND REPORTER AND FUSION

=> identif (s) (DNA (a) binding (a)  protein) and reporter and fusion
L8            0 IDENTIF (S) (DNA (A) BINDING (A) PROTEIN) AND REPORTER AND FUSIO
                N

=> identif? (s) (DNA (a) binding (a)  protein) and reporter and fusion
L9           25 IDENTIF? (S) (DNA (A) BINDING (A) PROTEIN) AND REPORTER AND
                FUSION

=> dup rem l9
PROCESSING COMPLETED FOR L9
L10          20 DUP REM L9 (5 DUPLICATES REMOVED)

=> t ti l10 1-20

L10  ANSWER 1 OF 20  WPIDS COPYRIGHT 2007       THE THOMSON CORP on STN

TI   New ERZFP polypeptides and polynucleotides useful for modulating the
     activity of estrogen receptor or for treating hormone-dependent types of
     cancer such as breast cancer, endometrial cancer or ovarian cancer

L10  ANSWER 2 OF 20  WPIDS COPYRIGHT 2007       THE THOMSON CORP on STN

TI   Novel compound comprising two portions obtained from steroids, hormones or
     drugs, joined by enzyme cleavable moiety such as amide or cephem moiety,
     useful for screening proteins capable of catalyzing bond cleavage

L10  ANSWER 3 OF 20  BIOSIS  COPYRIGHT (c) 2007 The Thomson Corporation  on STN
TI   Proteomic identification of TAL1/SCL-interacting proteins: ETO-2 and MTGR1
     interact with TAL1 in erythroid progenitors.

L10  ANSWER 4 OF 20  WPIDS COPYRIGHT 2007       THE THOMSON CORP on STN

TI   Novel human DNA binding protein involved in
     DNA replication useful as target in pharmaceutical assays for drugs
     designed to inhibit tumor cell division and for identifying
     compounds for modulating cell division

L10  ANSWER 5 OF 20  CAPLUS  COPYRIGHT 2007 ACS on STN DUPLICATE 1
TI   Creation and identification of proteins having new DNA-binding
     specificities using systems that avoid negative or positive selection
     pressure

L10  ANSWER 6 OF 20  WPIDS COPYRIGHT 2007       THE THOMSON CORP on STN
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TI New mutant RBP-J DNA binding protein capable of binding Notch or EBNA2 protein, useful for identifying and producing drugs for treating Epstein-Barr Virus infection or related diseases

L10 ANSWER 7 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

TI Regulating LRP5, LRP6 or HBM activity in a subject, useful for modulating lipid levels and/or bone mass, and for in treating bone mass disorders, e.g. osteoporosis, comprises administering a composition which modulates a Dkk activity

L10 ANSWER 8 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

TI Chemical or biological analysis, for diagnosing a disease or screening candidate drugs for treating a disease, by allowing species to participate in a chemical or biological interaction and identifying an oligonucleotide identifier

L10 ANSWER 9 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

TI Identifying agent interacting with Z-ring interacting protein A (ZipA), useful for inhibiting proliferation of bacteria having ZipA, comprises assessing ability of test agent to inhibit OrfE-ZipA interaction, in OrfE presence

L10 ANSWER 10 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

TI New chemical inducer of dimerization useful in methods of screening

L10 ANSWER 11 OF 20 MEDLINE on STN
TI Identification of a novel activation domain in the Notch-responsive transcription factor CSL.

L10 ANSWER 12 OF 20 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI Identification of a DNA-binding protein with multiple zinc fingers required for transcription of the secretin gene.

L10 ANSWER 13 OF 20 MEDLINE on STN
TI Cloning of a mouse glucocorticoid modulatory element binding protein, a new member of the KDWK family.

L10 ANSWER 14 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

TI New human XAF genes which interact with inhibitors of apoptosis proteins - useful as diagnostic reagents and for prevention and treatment of cancer, neurodegenerative disorders and apoptotic conditions including HIV

L10 ANSWER 15 OF 20 MEDLINE on STN DUPLICATE 2
TI Identification of human GC-box-binding zinc finger protein, a new Kruppel-like zinc finger protein, by the yeast one-hybrid screening with a GC-rich target sequence.

L10 ANSWER 16 OF 20 MEDLINE on STN
TI Characterization of the human thrombopoietin gene promoter. A possible role of an Ets transcription factor, E4TF1/GABP.

L10 ANSWER 17 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

TI Interaction trap systems using conformationally-constrained proteins -

useful for detection of protein interactions and for identification and isolation of interacting proteins

L10 ANSWER 18 OF 20 MEDLINE on STN
TI The upstream region of the SP-B gene: intrinsic promoter activity and glucocorticoid responsiveness related to a new DNA-binding protein.

L10 ANSWER 19 OF 20 CAPLUS COPYRIGHT 2007 ACS on STN
TI Screening for subunits of heterodimeric proteins and the genes encoding them

L10 ANSWER 20 OF 20 CAPLUS COPYRIGHT 2007 ACS on STN
TI Characterization of the Trichoderma reesei cbh2 promoter

=> d ibib abs l10 1-20

L10 ANSWER 1 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2005-092066 [10] WPIDS
DOC. NO. CPI: C2005-031148 [10]
TITLE: New ERZFP polypeptides and polynucleotides useful for modulating the activity of estrogen receptor or for treating hormone-dependent types of cancer such as breast cancer, endometrial cancer or ovarian cancer
DERWENT CLASS: B04; D16
INVENTOR: ALI S
PATENT ASSIGNEE: (UNLO-C) IMPERIAL COLLEGE INNOVATIONS LTD
COUNTRY COUNT: 105

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2005005473	A1	20050120	(200510)*	EN	108[19]	
AU 2003295093	A1	20050128	(200525)	EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2005005473	A1	WO 2003-GB5355	20031209
AU 2003295093	A1	AU 2003-295093	20031209

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2003295093	A1	Based on	WO 2005005473 A

PRIORITY APPLN. INFO: GB 2003-15827 20030705
AN 2005-092066 [10] WPIDS
AB WO 2005005473 A1 UPAB: 20050708
NOVELTY - A polypeptide, or its fragment, fusion or derivative, comprising a sequence of 1052 amino acids fully defined in the specification or an amino acid sequence having at least 45% identity with the sequence, for use in medicine, is new.
DETAILED DESCRIPTION - A polypeptide, or its fragment, fusion or derivative, comprising a sequence of 1052 (SEQ ID NO:1) amino acids fully defined in the specification or an amino acid sequence having at least 45% identity with (SEQ ID NO:1), for use in medicine, is new.
INDEPENDENT CLAIMS are also included for the following:

(1) a polynucleotide encoding the above polypeptide for use in medicine;

(2) an expression or gene therapy vector comprising the above polynucleotide;

(3) methods for modulating (e.g. inhibiting or promoting) the transcription factor activity of a transcription factor (e.g. a nuclear receptor DNA binding protein) in a cell;

(4) methods for identifying a compound that modulates (e.g. promotes or inhibits) the transcription factor activity of a transcription factor (e.g. a nuclear receptor DNA binding protein);

(5) a compound identified by the above method;

(6) methods for treating a patient with a hormone-dependent type of cancer or a patient in need of promotion of the activity of the transcription factor mentioned above;

(7) a transgenic animal overexpressing or underexpressing ERZFP or its fragment, variant, derivative or fusion;

(8) a pharmaceutical composition comprising the above polypeptide or polynucleotide; or the above compound and a drug that lowers estrogen levels (e.g. aromatase inhibitor or LHRH agonist) or an epidermal growth factor receptor (EGFR) antagonist or an inhibitor of ErbB2 or MEK signaling, or an antiestrogen; and a pharmaceutical carrier; and

(9) a kit of parts comprising the above compound or its fragment, and the above transcription factor (e.g. a nuclear receptor DNA binding protein or fragment); or a recombinant adenoviral vector and an ERZFP polypeptide and a hormone on which the hormone-dependent promoter is dependent (or its analogue that is able to promote transcription from the reporter, i.e. an agonist of the hormone receptor), and optionally also an antagonist of the hormone receptor and/or a partial antagonist of the hormone receptor.

ACTIVITY - Cytostatic. No biological data given.

MECHANISM OF ACTION - Gene therapy; Transcription factor-modulator.

USE - The compound (including the ERZFP polypeptide or its fragment, variant, fusion, derivative or peptidomimetic, the polynucleotide encoding the polypeptide, an antibody or its fragment that mimics the binding of the polypeptide to the transcription factor, a compound that inhibits the binding of the polypeptide ERZFP to the transcription factor, or a compound that reduces the amount of ERZFP in the cell) is useful in medicine or for modulating (e.g. inhibiting or promoting) the transcription factor activity of the transcription factor (claimed). The compound or polynucleotide is also used in manufacturing a medicament for treating a patient with a hormone-dependent type of cancer or a patient in need of promotion of the activity of the transcription factor (claimed). The recombinant adenoviral vector is used for identifying a compound that modulates or mimics the interaction between the ERZFP and the transcription factor (claimed). The composition and methods are used for treating hormone-dependent types of cancer such as breast cancer, endometrial cancer or ovarian cancer.

L10 ANSWER 2 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-440220 [41] WPIDS
CROSS REFERENCE: 2001-514515; 2002-147150
DOC. NO. CPI: C2004-164852 [41]
DOC. NO. NON-CPI: N2004-348416 [41]
TITLE: Novel compound comprising two portions obtained from steroids, hormones or drugs, joined by enzyme cleavable moiety such as amide or cephem moiety, useful for screening proteins capable of catalyzing bond cleavage
DERWENT CLASS: B04; D16; S03
INVENTOR: CORNISH V W
PATENT ASSIGNEE: (UYCO-C) UNIV COLUMBIA NEW YORK
COUNTRY COUNT: 1

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
US 20040106154	A1	20040603	(200441)*	EN	52[20]	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 20040106154	A1 CIP of	US 2000-490320	20000124
US 20040106154	A1 Div Ex	US 2001-768479	20010124
US 20040106154	A1	US 2003-705644	20031110

PRIORITY APPLN. INFO: US 2003-705644 20031110
US 2000-490320 20000124
US 2001-768479 20010124

AN 2004-440220 [41] WPIDS

CR 2001-514515; 2002-147150

AB US 20040106154 A1 UPAB: 20050530

NOVELTY - A compound (I) having specific formula comprises moieties capable of binding to a receptor and enzyme-cleavable moiety.

DETAILED DESCRIPTION - A compound (I) having formula H1-X-B-Y-H2, where H1 and H2 are same or different and capable of binding to a receptor which is same or different, X and Y are present or absent and, if present, each may be the same or different spacer moiety, and B is enzyme-cleavable moiety.

INDEPENDENT CLAIMS are also included for the following:

(1) a compound (II) having formula H1-X-B', where H1 is capable of binding to a receptor, X is a spacer moiety which is present or absent, and B' is moiety capable of binding to an enzyme;

(2) a complex (III) comprising (I) or (II) complexed to an enzyme;

(3) a composition (IV) comprising (I) and (II), or (III);

(4) screening (M1) proteins for the ability to catalyze bond cleavage, involves providing a cell that expresses a pair of fusion proteins which upon dimerization change a cellular readout, providing a compound which dimerizes the pair of fusion proteins, where the compound comprises two portions coupled by a bond that is cleavable by the protein to be screened, and screening for the cellular readout, where a change in the cellular readout indicates catalysis of bond cleavage by the protein to be screened;

(5) screening (M2) proteins for the ability to catalyze bond formation, involves carrying out the providing step of (M1), providing a first compound and second compound, each capable of binding to one of the pair of fusion proteins, where the first and second compound comprise a portion through which the first and second compounds are coupled by the action of the bond forming protein to be screened, and screening for the cellular readout, where a change in the cellular readout indicates catalysis of bond formation by the protein to be screened;

(6) screening (M3) a compound for the ability to inhibit an enzyme, involves screening for the activity of the enzyme by (M1) or (M2), and obtaining cells which express an active enzyme, and contacting the cells with the drug to be screened, where a change in the transcription of the reporter gene within the cell after contact with the drug indicates inhibition of the enzyme by the drug;

(7) a drug for the inhibition of an enzyme, selected by (M3);

(8) a protein with new catalytic activity evolved by using (M1) or (M2);

(9) an engineered enzyme having new substrate specificity evolved by using (M1) or (M2);

(10) evolving (M4) an enzyme that functions with a cofactor which

is different from the cofactor, which the natural coenzymes uses, involves evolving mutants of the natural coenzymes, and screening the mutants of the natural coenzyme by carrying out the steps of (M1) or (M2) in the presence of a cofactor different from the cofactor of the natural enzyme;

(11) an engineered enzyme that functions with a cofactor which is different from cofactors, the enzyme naturally uses, evolved by carrying out (M4);

(12) a compound (V) having formula H1-Y-H2, where H1 is methotrexate (Mtx) or its analog, H2 is capable of binding to a receptor, and Y is moiety providing a covalent linkage between H1 and H2, which is present or absent, and when absent, H1 is covalently linked to H2;

(13) a complex (VI) between (V) and a fusion protein which comprises a binding domain capable of binding to Mtx, where H1 of the compounds binds to the binding domain of the fusion protein;

(14) a complex between a compound having formulae (F2)-(F5), and fusion protein DHFR-LexA, or DHFR-B42;

(15) a cell comprising (VI);

(16) identifying (M5) a molecule that binds a known target in a cell from a pool candidate molecules, involves covalently bonding each molecule in the pool of candidate molecules to a Mtx moiety or its analog to form a screening molecule, introducing the screening molecule into a cell which expresses a first fusion protein comprising a binding domain capable of binding Mtx, a second fusion protein comprising the known target, and a reporter gene, where expression of the receptor gene is conditioned on the proximity of the first fusion protein to the second fusion protein, permitting the screening molecule to bind to the first fusion protein and to the second fusion to activate the expression of the reporter gene, selecting the cells that express the reporter gene, and identifying the small molecule that binds the known target; and

(17) identifying (M6) a protein target to which a molecule is capable of binding, involves providing a screening molecule comprising a Mtx moiety or its analog covalently bonded to a ligand which has specificity for an unknown protein target, carrying out the steps of introducing, permitting and selecting as mentioned in (M5), where the second fusion protein comprises an unknown protein target, and identifying the unknown protein target.

USE - (I) is useful in screening proteins having capability of catalyzing bond cleavage. (M1) or (M2) is useful for evolving a protein with a new catalytic activity, which involves screening the proteins derived from a library of proteins which are mutants of a known protein, by carrying out the steps of (M1) or (M2). (M1) or (M2) is useful for evolving an enzyme with a new substrate specificity, which involves screening the enzymes derived from a library of enzymes which are mutants of an enzyme with known substrate specificity, by carrying out the steps of (M1) or (M2). (V) is useful for dimerizing two fusion proteins inside a cell, which involves providing a cell that expresses a first fusion protein which comprises a binding domain that binds to H1 and second fusion protein which comprises a binding domain that binds to H2, and contacting (V) with the cell so as to dimerize the two fusion proteins. The first fusion protein or the second fusion protein is DHFR-(DNA-binding domain), DHFR-LexA, DHFR-(transcription activation domain), or DHFR-B42 (claimed).

DESCRIPTION OF DRAWINGS - The figure shows the method of screening glucosidase activity.

L10 ANSWER 3 OF 20 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2005:476425 BIOSIS
DOCUMENT NUMBER: PREV200510268329
TITLE: Proteomic identification of TAL1/SCL-interacting proteins: ETO-2 and MTGR1 interact with TAL1 in erythroid

progenitors.

AUTHOR(S): Cai, Ying [Reprint Author]; Xu, Zhixiong; Xie, Jingping; Koury, Mark J.; Hiebert, Scott W.; Brandt, Stephen J.

CORPORATE SOURCE: Vanderbilt Univ, Ctr Med, Dept Med, Nashville, TN USA

SOURCE: Blood, (NOV 16 2004) Vol. 104, No. 11, Part 1, pp. 105A. Meeting Info.: 46th Annual Meeting of the American-Society-of-Hematology. San Diego, CA, USA. December 04 -07, 2004. Amer Soc Hematol. CODEN: BLOOAW. ISSN: 0006-4971.

DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 16 Nov 2005
Last Updated on STN: 16 Nov 2005

AB The TAL1/SCL gene, originally identified from its involvement by a recurrent chromosomal translocation in T-cel acute lymphoblastic leukemia, encodes a basic helix-loop-helix (bHLH) transcription factor essential for hematopoietic andvascular development. Although TAL1 is believed to regulate transcription of specific sets of target genes, the mechanisms underlying TAL1-directed gene expression are poorly understood. Previous studies have shown, in fact, that it can act as either an activator or repressor depending on the coregulator(s) with which it interacts. To comprehensively identify TAL1's interaction partnersin erythroid cells, we stably expressed a tandem epitope-tagged mouse TAL1 protein in murine erythroleukemia (MEL) cells and determined the composition of affinity-purified TAL1-containing complexes by multidimensional mass spectrometry. From this analysis, we identified all known members of a TAL1-containing DNA-binding complex previously characterized in erythroid cells, including TAL1, its E protein DNA-binding partners, the zinc finger transcription factor GATA-1, the LIM-only protein LMO2, and the LIM domain-binding protein Ldb1, as well as proteins described to interact with GATA-1 (FOG-1), LMO2 (ELF2A2), and Ldb1 (SSDP2 and SSDP3). In addition, we identified a number of other DNA binding proteins, chromatin modifying proteins, and transcriptional regulators, including the ETO family members ETO-2 and MTGR1. TAL1 interaction with ETO-2 andMTGR1 was verified by coimmunoprecipitation analysis in MEL cells expressing these proteins at endogenous levels, in MEL cells stably expressing an epitope-tagged TAL1 protein, and in COS cells transiently transfected with TAL1 and ETO-2 or MTGR1 expression vectors. Mapping analysis with GAL4 fusion proteins identified the bHLH domain as the region in TAL1 responsible for interaction with these ETO family proteins. Significantly, expression of MTGR1 enhanced ETO-2 interaction with TAL1-GAL4 protein. Finally, transient transfection analysiswith a luciferase reporter construct linked to multiple GAL4 DNA binding sites showed greater than additive augmentation of TAL1-directed gene repression with coexpression of the two ETO-related proteins compared to that observed with ETO-2 or MTGR1 transfected individually. These results identify ETO-2 and MTGR1 as authentic TAL1 interacting proteins and suggest that a hetero-oligomeric complex of the two contributes to TAL1-directed repression in erythroid progenitors.

L10 ANSWER 4 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

ACCESSION NUMBER: 2003-290183 [28] WPIDS

DOC. NO. CPI: C2003-075479 [28]

TITLE: Novel human DNA binding protein involved in DNA replication useful as target in pharmaceutical assays for drugs designed to inhibit tumor cell division and for identifying compounds for modulating cell division

DERWENT CLASS: B04; D16

INVENTOR: CASPER J; LEFFAK M

PATENT ASSIGNEE: (CASP-I) CASPER J; (LEFF-I) LEFFAK M; (UYWR-N) UNIV

WRIGHT STATE
COUNTRY COUNT: 99

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2003020903	A2	20030313	(200328)*	EN	70[24]	
AU 2002324847	A1	20030318	(200452)	EN		
US 20040219554	A1	20041104	(200473)	EN		
AU 2002324847	A8	20051013	(200611)	EN		
US 20060084108	A1	20060420	(200627)	EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003020903	A2	WO 2002-US27809	20020830
US 20040219554	A1 Provisional	US 2001-316496P	20010831
AU 2002324847	A1	AU 2002-324847	20020830
AU 2002324847	A8	AU 2002-324847	20020830
US 20040219554	A1	WO 2002-US27809	20020830
US 20040219554	A1	US 2004-487964	20040226
US 20060084108	A1 Provisional	US 2001-316496P	20010831
US 20060084108	A1 Div Ex	WO 2002-US27809	20020830
US 20060084108	A1 Div Ex	US 2004-487964	20040226
US 20060084108	A1	US 2005-291360	20051201

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002324847 A1	Based on	WO 2003020903 A
AU 2002324847 A8	Based on	WO 2003020903 A

PRIORITY APPLN. INFO: US 2001-316496P 20010831
US 2004-487964 20040226
WO 2002-US27809 20020830
US 2005-291360 20051201

AN 2003-290183 [28] WPIDS
AB WO 2003020903 A2 UPAB: 20050528

NOVELTY - A human DNA binding protein (I) (DUE-B) involved in DNA replication, comprising a sequence of 209 amino acids defined in the specification, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) nucleic acid sequence (II) encoding (I);

(2) antibody (III), its derivative or fragment, binding to (I), and preventing the DNA binding protein from binding to a nucleic acid sequence; and

(3) gene therapy, by introducing into a cell an expression vector comprising (II), where (II) in the expression vector once introduced in the cell encodes a protein with a DNA binding activity.

ACTIVITY - Cytostatic.

MECHANISM OF ACTION - Gene therapy; Modulator of cell proliferation. No supporting data is given.

USE - (I) is useful in screening methods for identifying a compound binding to the amino acid sequence, and for identifying a compound modulating the binding of the DNA binding protein to a nucleic acid sequence. The method involves contacting (I) with a DNA in a medium, where the (I) is detectable and binding to the DNA, adding a compound to be screened for its capacity of modulating the

binding of amino acids to the DNA, to the medium, and detecting the effect on binding of the DNA binding protein to the DNA by the compound being screened. The compound identified inhibits cellular proliferation caused by cancer, or increases cellular proliferation. (I) is useful for screening compounds capable of modulating DNA replication, by contacting a compound to be screened with (I), in a medium, and determining binding of the compound to the DNA binding protein, where the detection of binding is indicative of the compound being capable of modulating DNA replication. Alternatively the method involves contacting in a medium, a compound to be screened with (I), adding DNA to the medium, and determining modulation of binding of the DNA binding protein to the DNA. (I) is further useful for screening compounds capable of modulating proliferation, especially cell proliferation. (III) is useful for preventing or decreasing cellular proliferation (all claimed). (I) is useful as a target in pharmaceutical assays for chemotherapeutic drugs designed to inhibit tumor cell division, as well as to identify other compounds for enhancing/retarding cell division.

L10 ANSWER 5 OF 20 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2002:391842 CAPLUS
DOCUMENT NUMBER: 136:396943
TITLE: Creation and identification of proteins having new DNA-binding specificities using systems that avoid negative or positive selection pressure
INVENTOR(S): Wise, John G.; Fromknecht, Katja
PATENT ASSIGNEE(S): Germany
SOURCE: PCT Int. Appl., 90 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2002040632	A2	20020523	WO 2001-US43107		20011116
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW					
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG					
AU 2002025623	A5	20020527	AU 2002-25623		20011116
US 2004161753	A1	20040819	US 2003-416708		20031031
PRIORITY APPLN. INFO.:			US 2000-249546P	P	20001117
			WO 2001-US43107	W	20011116

AB Methods are provided for identification and production of new DNA-binding proteins that up- or down-regulate the expression of pre-determined target genes. Such genes include DNA sequences that encode proteins that regulate such target genes as well as gene constructs and biol. materials that contain such DNA-binding proteins and/or their DNA sequences. Discovery methods also are provided for transcriptional promoters that allow identification of the desired target gene specific DNA-binding proteins, methods for targeting DNA-binding protein variants to the desired DNA-binding sequence, the methods for removing undesired DNA-binding protein variants from the total pool of all variants, as well as the media used for assaying in vivo DNA binding. The methods avoid the use of regular

neg. or pos. selection pressure to generate superior cell libraries of new sequences; a "genetically neutral" gene desirably used for selection in the invention is not very essential to cell growth and survival and/or does not measurably affect survival. The disadvantages of selection pressure on growth or replication are alleviated by relying on an operator, reporter, and/or separator gene product to distinguish cell clones of differing gene sequences without affecting cell survival or replication. A target DNA-binding sequence (a desired operator) is cloned adjacent to a structural gene used for screening and selection so that (1) the expression of the structural gene can be regulated through the binding of a DNA-binding protein variant to the operator sequence, and (2) the DNA-binding protein variants are expressed from DNA sequences that have been combinatorially mutated. The methods are exemplified by the generation and identification of 434 cro and NK2 homeodomain variants with new specificities for DNA regulatory sequences. The invention further encompasses kits for the identification and production of DNA-binding protein variants and/or their DNA sequences.

L10 ANSWER 6 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-140591 [13] WPIDS
DOC. NO. CPI: C2003-035790 [13]
TITLE: New mutant RBP-J DNA binding protein capable of binding Notch or EBNA2 protein, useful for identifying and producing drugs for treating Epstein-Barr Virus infection or related diseases
DERWENT CLASS: B04; D16
INVENTOR: KEMPKES B
PATENT ASSIGNEE: (GSFU-N) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI
COUNTRY COUNT: 98

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2002098918	A2	20021212	(200313)*	EN	28[6]	
AU 2002344370	A1	20021216	(200452)	EN		
AU 2002344370	A8	20051013	(200611)	EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002098918	A2	WO 2002-EP6002	20020531
AU 2002344370	A1	AU 2002-344370	20020531
AU 2002344370	A8	AU 2002-344370	20020531

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2002344370	A1	Based on	WO 2002098918 A
AU 2002344370	A8	Based on	WO 2002098918 A

PRIORITY APPLN. INFO: US 2001-295549P 20010605
AN 2003-140591 [13] WPIDS
AB WO 2002098918 A2 UPAB: 20050528
NOVELTY - A mutant RBP-J DNA binding protein (I) capable of binding Notch protein and comprising an amino acid sequence containing at least one mutation in the EBNA2 binding domain from amino acid positions 243-339, where the mutation renders the mutant RBP-J protein incapable of binding

EBNA2, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) a fusion protein (II) comprising the mutant RBP-J protein;

(2) a recombinant DNA molecule (IV) comprising a DNA sequence encoding (I) or the above fusion protein;

(3) a host cell (V) transformed with the recombinant DNA molecule;

(4) producing (I);

(5) isolating (M1) mutant RBP-J proteins incapable of binding EBNA2 but retaining the ability to bind Notch protein;

(6) a mutant RBP-J protein (VI) obtained by (M1) or its encoding DNA;

(7) identifying and isolating (M2) a drug for treating Epstein-Barr Virus (EBV)-infection or of a disorder or disease related to EBV-infection;

(8) obtaining (M3) a drug for treating EBV-infection or of a disorder or disease related to EBV-infection;

(9) a drug or a pro-drug (VII) obtained by (M3);

(10) a pharmaceutical composition (VIII) comprising the drug cited above; and

(11) treating (M4) an EBV-infection or a disorder or disease related to EBV-infection.

ACTIVITY - Virucide.

No biological data given.

MECHANISM OF ACTION - Gene therapy.

USE - The mutant RBP-J protein, the fusion protein, the recombinant DNA molecule, or the host cell, is useful for the identification of anti-EBV drugs (claimed). The RBP-J protein, Notch protein or EBNA2 protein, or their binding fragments, or the DNA encoding the protein or their fragments, is used for carrying out the methods cited above (claimed).

L10 ANSWER 7 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

ACCESSION NUMBER: 2003-129219 [12] WPIDS

CROSS REFERENCE: 2003-129214; 2003-129278; 2005-011698

DOC. NO. CPI: C2003-033012 [12]

TITLE: Regulating LRP5, LRP6 or HBM activity in a subject, useful for modulating lipid levels and/or bone mass, and for in treating bone mass disorders, e.g. osteoporosis, comprises administering a composition which modulates a Dkk activity

DERWENT CLASS: B04; D16; P14

INVENTOR: ALLEN K; ALLEN K M; ANISOWICZ A; BHAT B M; DAMAGNEZ V; ROBINSON J A; YAWORSKY P J

PATENT ASSIGNEE: (ALLE-I) ALLEN K M; (ANIS-I) ANISOWICZ A; (DAMA-I) DAMAGNEZ V; (GENO-N) GENOME THERAPEUTICS CORP; (AMHP-C) WYETH

COUNTRY COUNT: 99

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2002092015	A2	20021121	(200312)*	EN	173[28]	
US 20040038860	A1	20040226	(200416)	EN		
EP 1395285	A2	20040310	(200418)	EN		
AU 2002342734	A1	20021125	(200452)	EN		
BR 2002009836	A	20041207	(200507)	PT		
JP 2005512508	W	20050512	(200532)	JA	309	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002092015 A2		WO 2002-US15982	20020517
AU 2002342734 A1		AU 2002-342734	20020517
BR 2002009836 A		BR 2002-9836	20020517
EP 1395285 A2		EP 2002-744162	20020517
JP 2005512508 W		JP 2002-588934	20020517
US 20040038860 A1		WO 2002-US15982	20020517
EP 1395285 A2		WO 2002-US15982	20020517
BR 2002009836 A		WO 2002-US15982	20020517
JP 2005512508 W		WO 2002-US15982	20020517
US 20040038860 A1		US 2002-182936	20020802

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1395285 A2	Based on	WO 2002092015 A
AU 2002342734 A1	Based on	WO 2002092015 A
BR 2002009836 A	Based on	WO 2002092015 A
JP 2005512508 W	Based on	WO 2002092015 A

PRIORITY APPLN. INFO: US 2002-361293P 20020304
US 2001-291311P 20010517
US 2002-353058P 20020201
US 2002-182936 20020802

AN 2003-129219 [12] WPIDS

CR 2003-129214; 2003-129278; 2005-011698

AB WO 2002092015 A2 UPAB: 20060118

NOVELTY - Regulating LRP5, LRP6 or HBM activity in a subject comprising administering a composition which modulates a Dkk activity, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) regulating Dkk-Wnt pathway activity in a subject;

(2) modulating bone mass in a subject;

(3) modulating lipid levels in a subject;

(4) diagnosing low or high bone mass and/or high or low lipid levels in a subject;

(5) screening for a compound which modulates the interaction of Dkk with LRP5, LRP6, HBM or a Dkk-binding fragment of LRP5, LRP6 or HBM;

(6) screening a compound which modulates the interaction of Dkk with a Dkk interacting protein;

(7) a composition comprising an LRP5, LRP6 or HBM activity-modulating compound, and a pharmaceutical carrier;

(8) a pharmaceutical composition a compound which modulate Dkk and LRP5/LRP6/HBM interactions;

(9) identifying binding partners for a Dkk protein or compounds which modulate Dkk and/or LRP5/LRP6/HBM interactions;

(10) a nucleic acid encoding a Dkk interacting protein peptide aptamer comprising a nucleic acid encoding a scaffold protein in-frame with the activation domain of Gal4 or Lex A that is in frame with a nucleic acid that encodes a Dkk interacting protein amino acid sequence;

(11) a vector comprising the nucleic acid of (10);

(12) detecting a modulatory activity of a compound on the binding interaction of a first peptide and a second peptide of a peptide-binding pair that binds through extracellular interaction in their natural environment;

(13) a transgenic animal where Dkk-1 is knocked out in a tissue-specific fashion;

(14) identifying potential compounds which modulate Dkk activity;

(15) a peptide aptamer comprising one of 22 13-32 residue amino acid sequences, given in the specification;

(16) an antibody or antibody fragment which recognizes and binds to one or more of 18 13-17 residue amino acid sequences, given in the specification;

(17) identifying Dkk interacting proteins which modulate the interaction of Dkk with the Wnt signaling pathway;

(18) identifying compounds which modulate Dkk and LRP5/LRP6/HBM interactions;

(19) identifying compounds which modulate the interaction of Dkk with the Wnt signaling pathway;

(20) testing compounds that modulate Dkk-mediated activity in a mammal;

(21) screening for compounds or compositions which modulate the interaction of Dkk and a Dkk interacting protein; and

(22) an antibody or antibody fragment which recognizes and binds to a sequence selected from 18 peptide sequences given in the specification.

ACTIVITY - Osteopathic; Antiinflammatory; Antiarthritic.

No biological data is given.

MECHANISM OF ACTION - Dkk modulator.

USE - The method is useful for modulating lipid levels and/or bone mass, and is useful in treating or diagnosing abnormal lipid levels and bone mass disorders, such as osteoporosis, bond fracture, age-related loss of bone, a chondrodystrophy, drug-induced bone disorder, high bone turnover, hypercalcemia, hyperostosis, osteogenesis, imperfecta, osteomalacia, osteomyelitis, Paget's disease, osteoarthritis, and rickets. Modulators of Dkk activity are useful for as reagents in studying bone mass and lipid level modulation, in modulating Wnt signaling, or treating Dkk-mediated disorders.

L10 ANSWER 8 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN

ACCESSION NUMBER: 2002-608527 [65] WPIDS

DOC. NO. CPI: C2002-172128 [65]

TITLE: Chemical or biological analysis, for diagnosing a disease or screening candidate drugs for treating a disease, by allowing species to participate in a chemical or biological interaction and identifying an oligonucleotide identifier

DERWENT CLASS: B04; D16

INVENTOR: BAMBAD R S; BAMDAD C C; BAMDAD R S; SHENDELMAN S B

PATENT ASSIGNEE: (BAMD-I) BAMDAD C C; (BAMD-I) BAMDAD R S; (MINE-N) MINERVA BIOTECHNOLOGIES CORP

COUNTRY COUNT: 98

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2002061129	A2	20020808	(200265)*	EN	73[19]	
US 20020164611	A1	20021107	(200275)	EN		
EP 1348034	A2	20031001	(200365)	EN		
AU 2002248159	A1	20020812	(200427)	EN		
US 20050053964	A1	20050310	(200519)	EN		
JP 2005513999	W	20050519	(200538)	JA	46	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002061129	A2	WO 2001-US45845	20011115
US 20020164611	A1 Provisional	US 2000-248863P	20001115
US 20050053964	A1 Provisional	US 2000-248863P	20001115
US 20020164611	A1 Provisional	US 2000-252650P	20001122
US 20050053964	A1 Provisional	US 2000-252650P	20001122

US 20020164611 A1	Provisional	US 2001-276995P 20010319
US 20050053964 A1	Provisional	US 2001-276995P 20010319
US 20020164611 A1	Provisional	US 2001-302231P 20010629
US 20050053964 A1	Provisional	US 2001-302231P 20010629
US 20020164611 A1	Provisional	US 2001-326937P 20011003
US 20020164611 A1	Provisional	US 2001-327089P 20011003
US 20050053964 A1	Provisional	US 2001-326937P 20011003
US 20050053964 A1	Provisional	US 2001-327089P 20011003
EP 1348034 A2		EP 2001-997037 20011115
US 20020164611 A1		US 2001-4275 20011115
US 20050053964 A1	Cont of	US 2001-4275 20011115
EP 1348034 A2		WO 2001-US45845 20011115
JP 2005513999 W		WO 2001-US45845 20011115
AU 2002248159 A1		AU 2002-248159 20011115
JP 2005513999 W		JP 2002-561064 20011115
US 20050053964 A1		US 2004-756802 20040113

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1348034 A2	Based on	WO 2002061129 A
AU 2002248159 A1	Based on	WO 2002061129 A
JP 2005513999 W	Based on	WO 2002061129 A

PRIORITY APPLN. INFO: US 2001-327089P 20011003
US 2000-248863P 20001115
US 2000-252650P 20001122
GB 2001-1054 20010115
US 2001-276995P 20010319
US 2001-302231P 20010629
US 2001-326937P 20011003

AN 2002-608527 [65] WPIDS

AB WO 2002061129 A2 UPAB: 20060120

NOVELTY - Chemical or biological analysis, by allowing a species, immobilized relative to a surface, to participate in a chemical or biological interaction, and determining participation of the chemical or biological species in the chemical or biological interaction by identifying an oligonucleotide identifier that encodes the chemical or biological species associated with the surface, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a kit comprising:

(a) an article having a surface;

(b) a chemical or biological species, able to participate in a chemical or biological interaction, fastened to or adapted to be fastened to the surface; and

(c) an oligonucleotide identifier fastened to or adapted to be fastened to the surface;

(2) a kit comprising several particles each carrying a chemical or biological functionality allowing it to fasten to a binding partner, and each carrying an identical oligonucleotide linker constructed for attachment to a complementary oligonucleotide fastened to an oligonucleotide identifier;

(3) a kit comprising:

(a) a surface;

(b) a protein immobilized or adapted to be immobilized relative to the surface; and

(c) an oligonucleotide identifier that codes for the protein, immobilized or adapted to be immobilized relative to the surface;

(4) a kit comprising:

(a) a polymer or dendrimer;

(b) a protein immobilized or adapted to be immobilized relative to the polymer or dendrimer; and

(c) an oligonucleotide identifier that codes for the protein, immobilized or adapted to be immobilized relative to the polymer or dendrimer;

(5) a kit comprising:

(a) a protein and an oligonucleotide identifier that codes for the protein, immobilized or adapted to be immobilized relative to each other; and

(b) an entity carrying immobilized to it a binding partner of the protein;

(6) a kit comprising:

(a) at least one colloid particle;

(b) at least one magnetic bead;

(c) at least one protein recognition motif adapted for immobilization to at least one colloid particle; and

(d) an uncharacterized protein or drug adapted for immobilization to at least one bead;

(7) a composition comprising:

(a) a chemical or biological species, able to participate in a chemical or biological interaction, or a protein;

(b) a linker species that is not a ribosome; and

(c) an oligonucleotide identifier, where each of the chemical or biological species and the oligonucleotide identifier is fastened to or adapted to be fastened to the linker species, or an oligonucleotide identifier that encodes for the protein, where each of the protein and the oligonucleotide identifier is immobilized or adapted to be immobilized relative to the linker species;

(8) a composition comprising a protein and an oligonucleotide identifier that codes for the protein, immobilized or adapted to be immobilized relative to each other;

(9) a method comprising expressing a protein with an oligonucleotide and immobilizing the protein and the oligonucleotide relative to each other;

(10) generating a library of nucleic acids or plasmids that contain components of a cDNA library and:

(a) a functionality to facilitate binding to a surface;

(b) a functionality the products of which are used in an in vitro assay;

(c) sequences to which nucleic acid binding proteins bind; or

(d) sequences that encode a DNA binding domain and sequences to which the encoded DNA binding domain binds, where the binding motif sequences are not in proximity to a reporter gene;

(11) exposing several colloid particles, each carrying an immobilized protein recognition motif, to a bead carrying an immobilized, uncharacterized protein or drug, and determining immobilization of at least one particle to the bead via interaction between the protein recognition motif and the uncharacterized protein or drug.

USE - The methods are useful for chemical and biological analyses, analyzing for the presence of species associated with a disease, diagnosing a disease, or screening of candidate drugs for treating e.g. neurodegenerative diseases.

ADVANTAGE - The present methods are simple, extremely sensitive and utilize readily-available components. The present methods, assays and components provide rapid, high throughput, specific and sensitive detection and analysis of biomolecular and chemical interactions. Large numbers of interactions can be screened simultaneously, as opposed to prior techniques.

L10 ANSWER 9 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2002-657425 [70] WPIDS
DOC. NO. CPI: C2002-184416 [70]

TITLE: Identifying agent interacting with Z-ring interacting protein A (ZipA), useful for inhibiting proliferation of bacteria having ZipA, comprises assessing ability of test agent to inhibit OrfE-ZipA interaction, in OrfE presence

DERWENT CLASS: B04; D16

INVENTOR: HANEY S; HANEY S A

PATENT ASSIGNEE: (HANE-I) HANEY S A; (AMHP-C) WYETH

COUNTRY COUNT: 96

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2002051977	A2	20020704	(200270)*	EN	51[6]	
US 20030078191	A1	20030424	(200330)	EN		
AU 2002232661	A1	20020708	(200427)	EN		
AU 2002232661	A8	20051013	(200611)	EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002051977	A2	WO 2001-US49233	20011217
US 20030078191	A1 Provisional	US 2000-257647P	20001222
US 20030078191	A1	US 2001-24644	20011217
AU 2002232661	A1	AU 2002-232661	20011217
AU 2002232661	A8	AU 2002-232661	20011217

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2002232661	A1	Based on	WO 2002051977 A
AU 2002232661	A8	Based on	WO 2002051977 A

PRIORITY APPLN. INFO: US 2000-257647P 20001222
US 2001-24644 20011217

AN 2002-657425 [70] WPIDS

AB WO 2002051977 A2 UPAB: 20050527

NOVELTY - Identifying (M1) an agent interacting with Z-ring interacting protein A (ZipA), comprises (a) contacting candidate agent (I) with ZipA, in presence of OrfE (product of kil locus of Rac (a cryptic prophage)) which is a 25 kb fragment located at min 29.5 in many Escherichia coli K-12 strains); and (b) assessing ability of (I) to inhibit OrfE-ZipA interaction.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an agent (II) identified by (M1); and

(2) a complex (III) comprising OrfE and ZipA.

ACTIVITY - Antibacterial.

No supporting data is given.

MECHANISM OF ACTION - Inhibitor of proliferation of bacterium containing ZipA; ZipA- OrfE interaction inhibitor where ZipA is an essential component of cell division machinery of gram negative bacteria (all claimed).

USE - The method is useful in identifying an agent (II) that interacts with ZipA. (II) is useful for inhibiting proliferation of a bacterium containing ZipA, such as Escherichia coli. (II) is also useful for treating bacterial infection in a subject infected with a bacterium containing ZipA such as E.coli (all claimed). The OrfE-ZipA interaction and the OrfE-ZipA complex may be used as tools in the development of drug screens, as a target for small molecule inhibitors that can act as

antimicrobial agents, and as basis for peptidomimetics. Such drugs, inhibitors, and peptidomimetics may be useful for treating a subject infected with a bacterium.

ADVANTAGE - The design and synthesis of an inhibitor of ZipA biological activity is relatively simple, since (a) the OrfE binding site of ZipA is a relatively small peptide sequence (contained within residues 176-328 of ZipA); and (b) the substrate of the OrfE-binding site of ZipA is OrfE - a small, 78-residue protein of known molecular structure. Also ZipA is commonly found in Gram-negative bacteria, and is not found in human cells; therefore, a ZipA inhibitor would not be expected to display toxicity for human cells.

L10 ANSWER 10 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2001-514515 [56] WPIDS
CROSS REFERENCE: 2002-147150; 2004-440220
DOC. NO. CPI: C2001-153746 [56]
TITLE: New chemical inducer of dimerization useful in methods of screening
DERWENT CLASS: B01; B02; B04
INVENTOR: CORNISH V W
PATENT ASSIGNEE: (UYCO-C) UNIV COLUMBIA NEW YORK
COUNTRY COUNT: 92

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2001053355	A1	20010726	(200156)*	EN	122[23]	
AU 2001029741	A	20010731	(200171)	EN		
EP 1254179	A1	20021106	(200281)	EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001053355	A1	WO 2001-US2285	20010124
AU 2001029741	A	AU 2001-29741	20010124
EP 1254179	A1	EP 2001-942644	20010124
EP 1254179	A1	WO 2001-US2285	20010124

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001029741	A	Based on	WO 2001053355 A
EP 1254179	A1	Based on	WO 2001053355 A

PRIORITY APPLN. INFO: US 2000-490320 20000124
AN 2001-514515 [56] WPIDS
CR 2002-147150; 2004-440220
AB WO 2001053355 A1 UPAB: 20060117
NOVELTY - A chemical inducer of dimerization (I) is new.
DETAILED DESCRIPTION - Chemical inducers of dimerization of formula (I) are new.
H1-X-B'-Y-H2'' (I)
H1 and H2'' = substituent capable of binding to a receptor;
X and Y' = spacer moiety or are absent;
B' = enzyme-cleavable moiety;
INDEPENDENT CLAIMS are also included for the compounds of formula H1'-X-B'', an intermediate in the preparation of (I) and of formula H1'-Y''-H2'.
B'' = moiety capable of binding to an enzyme;

H1' = methotrexate or its analog;
H2' = moiety capable of binding to a receptor;
Y'' = moiety providing a covalent linkage between H1' and H2' or is absent.

USE - A method of screening proteins for the ability to catalyze bond cleavage comprises:

(a) providing a cell that expresses a pair of fusion proteins which change a cellular readout on dimerization;

(b) providing a compound ((I) or H1-X-B'') which dimerizes the proteins, the compound comprising two portions coupled by a bond cleavable by the protein to be screened; and

(c) screening for the cellular readout, a change in the readout indicating catalysis of bond cleavage by the protein to be screened. The cellular readout is reconstitution of enzymatic activity.

A method of screening proteins for the ability to catalyze bond formation comprises:

(a) providing a cell that expresses a pair of fusion proteins which change a cellular readout on dimerization;

(b) providing a first compound and a second compound (one of which is (I) in which H1 or H2'' represents dexamethasone, 3,5,3'-triiodothyronine, trans-retinoic acid, biotin, coumermycin, tetracycline, lactose, methotrexate or FK506 or its analog) each capable of binding to one of the pair of fusion proteins, the first and second compound comprising a portion through which the first and second compounds are coupled by the action of the bond forming protein to be screened; and

(c) screening for the cellular readout, a change in the readout indicating catalysis of bond formation by the protein to be screened. The cellular readout is enzyme activity.

A method of screening a compound for the ability to inhibit an enzyme comprises screening for activity of the enzyme by the method of screening for the ability to catalyze bond cleavage or bond formation and obtaining cells which express an active enzyme then contacting the cells with the drug to be screened, a change in the transcription of the reporter gene within the cell after contact with the drug indicating inhibition of the enzyme by the drug. A method of evolving a protein with a new catalytic activity comprises screening proteins from a library of proteins which are mutants of a known protein for the ability to catalyze bond cleavage or bond formation. A method of evolving an enzyme with a new substrate specificity comprises screening enzymes from a library of enzymes which are mutants of an enzyme with known substrate specificity for the ability to catalyze bond cleavage or bond formation.

A method for evolving an enzyme that functions with a cofactor different from the cofactor the natural coenzyme uses comprises evolving mutants for the natural coenzyme and screening the mutants for the ability to catalyze bond cleavage or bond formation in the presence of a cofactor different from the cofactor of the natural enzyme.

A method of dimerizing two fusion proteins inside a cell using the compound of formula H1-Y'-H2'' comprises providing a cell that expresses a first fusion protein which comprises a binding domain that binds to H1 and second fusion protein which comprises a binding domain that binds to H2'' and contacting H1-Y'-H2'' with the cell so as to dimerize the two fusion proteins. The first or second fusion protein is DHFR-(DNA-binding domain), DHFR-LexA, DHFR-(transcription activation domain) or DHFR-B42.

A method for identifying a molecule that binds a known target in a cell from a pool of candidate molecules comprises:

(a) covalently bonding each molecule in the pool of candidate molecule to a methotrexate moiety or an analog of methotrexate to form a screening molecule;

(b) introducing the screening molecule into a cell which expresses a first fusion protein comprising a binding domain capable of binding methotrexate, a second fusion protein comprising the

known target and a reporter gene in which expression of the reporter gene is conditioned on the proximity of the first fusion protein to the second fusion protein;

(c) permitting the screening molecule to bind to the first fusion protein and to the second fusion protein so as to activate the expression of the reporter gene;

(d) selecting which cell expresses the reporter gene; and

(e) identifying the small molecule that binds the known target. The cell is selected from insect cells, yeast cells, mammalian cells and their lysates. The first or second fusion protein comprises a transcription module selected from a DNA binding protein and a transcriptinal activator. The molecule is obtained from a combinatorial library.

Steps (b) to (e) are repeated in the presence of a preparation of random small molecules for competitive binding with the hybrid ligand so as to identify a molecule capable of competitively binding the known target.

L10 ANSWER 11 OF 20 MEDLINE on STN
ACCESSION NUMBER: 2001296835 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11376147
TITLE: Identification of a novel activation domain in the Notch-responsive transcription factor CSL.
AUTHOR: Tang Z; Kadesch T
CORPORATE SOURCE: Department of Genetics, University of Pennsylvania School of Medicine, Philadelphia, PA 19104-6145, USA.
CONTRACT NUMBER: R01 GM58228 (NIGMS)
SOURCE: Nucleic acids research, (2001 Jun 1) Vol. 29, No. 11, pp. 2284-91.
Journal code: 0411011. E-ISSN: 1362-4962.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 25 Jun 2001
Last Updated on STN: 25 Jun 2001
Entered Medline: 21 Jun 2001

AB CSL is the primary target of the Notch signaling pathway in mammalian cells. It is a DNA binding protein that generally represses transcription in the absence of Notch signaling and activates transcription upon formation of a ternary complex with NICD, the protease-generated intracellular domain of NOTCH: Previous mapping experiments identified the central third of CSL as both necessary and sufficient for DNA binding and activation by NOTCH: Here we show that CSL promotes transcription in 293T cells in the absence of added NICD and that this activity requires both the central domain plus the C-terminal third of the protein. Evidence is presented that argues against a contribution of endogenous NICD and instead supports the possibility that distinct coactivators may directly stimulate the activity of CSL in a cell type-specific manner. This conclusion supports a recent finding that Drosophila CSL (Suppressor of Hairless) can also mediate transcriptional activation in the absence of NOTCH:

L10 ANSWER 12 OF 20 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2002:175701 BIOSIS
DOCUMENT NUMBER: PREV200200175701
TITLE: Identification of a DNA-binding protein with multiple zinc fingers required for transcription of the secretin gene.
AUTHOR(S): Ray, Subir K. [Reprint author]; Leiter, Andrew B. [Reprint

author]
CORPORATE SOURCE: New England Medical Ctr, Boston, MA, USA
SOURCE: Gastroenterology, (April, 2001) Vol. 120, No. 5 Supplement 1, pp. A.22. print.
Meeting Info.: 102nd Annual Meeting of the American Gastroenterological Association and Digestive Disease Week. Atlanta, Georgia, USA. May 20-23, 2001. American Gastroenterological Association; American Association for the Study of Liver Diseases; American Society for Gastrointestinal Endoscopy; Society for Surgery of the Alimentary Tract.
CODEN: GASTAB. ISSN: 0016-5085.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 6 Mar 2002
Last Updated on STN: 6 Mar 2002

L10 ANSWER 13 OF 20 MEDLINE on STN
ACCESSION NUMBER: 2000158851 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10692587
TITLE: Cloning of a mouse glucocorticoid modulatory element binding protein, a new member of the KDWK family.
AUTHOR: Jimenez-Lara A M; Heine M J; Gronemeyer H
CORPORATE SOURCE: Institut de Genetique et de Biologie Moleculaire et Cellulaire, CNRS/INSERM/ULP, P.O. Box 163, 67404, Illkirch, France.
SOURCE: FEBS letters, (2000 Feb 25) Vol. 468, No. 2-3, pp. 203-10.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 13 Apr 2000
Last Updated on STN: 13 Apr 2000
Entered Medline: 3 Apr 2000
AB A mouse cDNA that encodes a nuclear DNA binding protein was identified by yeast two-hybrid screening using the activation domain 2 of the nuclear receptor coactivator TIF2 as a bait. BLAST analysis revealed that the identified cDNA encodes a KDWK domain and contains sequences almost identical to three tryptic peptides of rat GMEB-1 which together with the GMEB-2 heterodimeric partner binds to the GME/CRE sequence (glucocorticoid modulatory element) of the tyrosine aminotransferase (TAT) promoter. Mouse GMEB-1 is ubiquitously expressed in all the tissues examined. In vitro translated mGMEB-1 bound specifically to GME oligonucleotides, either alone or as a heterodimer with rGMEB-2. Transient transfection experiments with TAT promoter reporter genes suggest a potential role for mGMEB-1 as a transcriptional regulator of the TAT promoter.

L10 ANSWER 14 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 1999-083565 [08] WPIDS
DOC. NO. CPI: C1999-025342 [08]
DOC. NO. NON-CPI: N1999-060285 [08]
TITLE: New human XAF genes which interact with inhibitors of apoptosis proteins - useful as diagnostic reagents and for prevention and treatment of cancer, neurodegenerative disorders and apoptotic conditions including HIV
DERWENT CLASS: B04; D16; P14; S03
INVENTOR: BAIRD S; KORNELUK R; KORNELUK R G; LISTON P; MACKENZIE A E; TAMAI K

PATENT ASSIGNEE: (AEGE-N) AEGERA THERAPEUTICS INC; (APOP-N) APOPTOGEN INC; (UYOT-N) UNIV OTTAWA

COUNTRY COUNT: 28

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
EP 892048	A2	19990120	(199908)*	EN	101[40]	
JP 11032780	A	19990209	(199916)	JA	64	
CA 2225187	A	19990114	(199926)	EN		
US 6107088	A	20000822	(200042)	EN		
US 6495339	B1	20021217	(200307)	EN		
US 20030215824	A1	20031120	(200377)	EN		
US 6946544	B2	20050920	(200562)	EN		
US 20060040862	A1	20060223	(200615)	EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 892048	A2	EP 1998-113003	19980713
US 6107088	A Provisional	US 1997-52402P	19970714
US 6495339	B1 Provisional	US 1997-52402P	19970714
US 20030215824	A1 Provisional	US 1997-52402P	19970714
US 6946544	B2 Provisional	US 1997-52402P	19970714
US 6107088	A Provisional	US 1997-54491P	19970801
US 6495339	B1 Provisional	US 1997-54491P	19970801
US 20030215824	A1 Provisional	US 1997-54491P	19970801
US 6946544	B2 Provisional	US 1997-54491P	19970801
US 6107088	A Provisional	US 1997-56338P	19970818
US 6495339	B1 Provisional	US 1997-56338P	19970818
US 20030215824	A1 Provisional	US 1997-56338P	19970818
US 6946544	B2 Provisional	US 1997-56338P	19970818
JP 11032780	A	JP 1997-252889	19970901
CA 2225187	A	CA 1998-2225187	19980227
US 6107088	A	US 1998-100391	19980619
US 6495339	B1 Div Ex	US 1998-100391	19980619
US 20030215824	A1 Div Ex	US 1998-100391	19980619
US 6946544	B2 Div Ex	US 1998-100391	19980619
US 6495339	B1	US 2000-616614	20000714
US 20030215824	A1 Cont of	US 2000-616614	20000714
US 6946544	B2 Cont of	US 2000-616614	20000714
US 20030215824	A1	US 2002-288273	20021105
US 6946544	B2	US 2002-288273	20021105
US 20060040862	A1 Provisional	US 1997-52402P	19970714
US 20060040862	A1 Provisional	US 1997-54491P	19970801
US 20060040862	A1 Provisional	US 1997-56338P	19970818
US 20060040862	A1 Div Ex	US 1998-100391	19980619
US 20060040862	A1 Cont of	US 2000-616614	20000714
US 20060040862	A1 Div Ex	US 2002-288273	20021105
US 20060040862	A1	US 2005-205225	20050816

FILING DETAILS:

PATENT NO	KIND		PATENT NO	
US 6495339	B1	Div ex	US 6107088	A
US 20030215824	A1	Div ex	US 6107088	A
US 6946544	B2	Div ex	US 6107088	A
US 20030215824	A1	Cont of	US 6495339	B
US 6946544	B2	Cont of	US 6495339	B

US 20060040862	A1	Div ex	US 6107088	A
US 20060040862	A1	Cont of	US 6495339	B
US 20060040862	A1	Div ex	US 6946544	B

PRIORITY APPLN. INFO: US 1997-56338P 19970818
US 1997-52402P 19970714
US 1997-54491P 19970801
US 1998-100391 19980619
US 2000-616614 20000714
US 2002-288273 20021105
US 2005-205225 20050816

AN 1999-083565 [08] WPIDS

AB EP 892048 A2 UPAB: 20060114

A substantially pure nucleic acid (I) encoding an XAF polypeptide (II), which interacts with inhibitors of apoptosis proteins (IAPs) and induce apoptosis is new. Also claimed are: (1) an antisense nucleic acid corresponding to at least 10 nucleotides of (I), able to decrease XAF biological activity; (2) a vector comprising (I), for XAF polypeptide expression; (3) a cell containing (I); (4) a transgenic animal generated from a cell genetically engineered to lack (I), unable to express (II); (5) an antibody for XAF polypeptide (II) or a fragment of (II); (6) methods for increasing apoptosis in a cell, comprising administering (i) XAF polypeptide (II); or (ii) a transgene encoding (II) or a fragment into a mammal cell; (7) a method of inhibiting apoptosis in a cell by administering a compound which decreases XAF biological activity; (8) methods for identifying a compound that modulates apoptosis by contacting a cell comprising: (i) a reporter gene operably linked to an XAF gene promoter; or (ii) a TRAF and an XAF polypeptide and a reporter gene operably linked to DNA comprising an NF-kB binding site; or (iii) a TRAF, an IAP and an XAF polypeptide, and a reporter gene operably linked to DNA comprising an NF-kB binding site; with candidate compound and measuring change in expression; (9) methods for detecting apoptosis modulating compounds by exposing a cell having: (i) a reporter gene operably linked to a DNA-binding-protein recognition site (III); and (ii) a first XAF fusion gene (I) bonded to a binding moiety which binds (III); and (iii) a second XAF or IAP fusion protein with gene activating moieties; and measuring change in reporter gene expression; (10) a method as in (9), where the first fusion gene comprises an IAP polypeptide, and the second comprises XAF (II); and (11) methods for detecting apoptosis modulating compounds by: (i) immobilising an XAF polypeptide on a solid-phase substrate; (ii) contacting with an XAF or IAP polypeptide; (iii) adding the candidate compound, and measuring the binding; and (12) a method as (11), where the first polypeptide is IAP, and the second is XAF.

USE - The new XAF gene and its variants are useful for identifying compounds which modulate (increase or decrease) apoptosis by monitoring expression of XAF in the presence of a candidate (claimed). These compounds and XAF antibodies are useful for treating diseases related to overexpression of XAF (which causes cell death) e.g. neurodegenerative disorders, and activating compounds and XAF polypeptides can be administered to treat impaired apoptosis diseases caused by underexpression of XAF e.g. cancer. Gene therapy can also be used to treat the above conditions by administering the vector comprising an XAF gene (I) or the XAF antisense nucleic acid. Gene therapy or administration of XAF polypeptides are useful for preventing apoptotic conditions in patients with a degenerative disease, is HIV positive, or has a mutated XAF gene or aberrant XAF expression. The new XAF gene is useful for diagnosing a mammal with a disease related to altered apoptosis expression by determining the presence of a gene mutation, or measuring gene activity levels (claimed). The XAF expressing cells are useful for studies of XAF genes and gene products, especially for identifying domains of biological

activity, and for production of large amounts of normal and mutant protein. XAF antibodies are useful for detecting XAF proteins, and are useful in therapeutic treatments by inhibiting the biological activity of the proteins, or coupling to active compounds for targeting to specific tissues. XAF nucleic acids are useful for identifying homologous clones and sequences using low stringency hybridisation.

L10 ANSWER 15 OF 20 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 1999332089 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10405178
TITLE: Identification of human GC-box-binding zinc finger protein, a new Kruppel-like zinc finger protein, by the yeast one-hybrid screening with a GC-rich target sequence.
AUTHOR: Lisowsky T; Polosa P L; Sagliano A; Roberti M; Gadaleta M N; Cantatore P
CORPORATE SOURCE: Botanisches Institut, Heinrich-Heine-Universitat Dusseldorf, Germany.
SOURCE: FEBS letters, (1999 Jun 25) Vol. 453, No. 3, pp. 369-74. Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ132591; GENBANK-AJ132592
ENTRY MONTH: 199908
ENTRY DATE: Entered STN: 16 Aug 1999
Last Updated on STN: 16 Aug 1999
Entered Medline: 5 Aug 1999
AB A new human zinc finger DNA-binding protein was identified by using a yeast one-hybrid selection system. Two versions of the cDNA, encoding the same protein, were detected that differ for a 584 bp extension at the 5' region. Sequence analysis showed that the longer clone is a full length version containing part of the 5' untranslated region. The smaller version was fused in frame with the yeast GAL4 activation domain whereas the 5' region of the longer clone displayed a stop codon interrupting the fusion with the GAL4 domain. Nevertheless, this clone activated the yeast HIS3 reporter gene with the same efficiency as the smaller version. Sequence comparison of the derived protein with the database showed that it belongs to a family of zinc finger DNA-binding proteins which regulate the expression of genes involved in cell proliferation. Expression of the protein in an in vitro system, DNA-binding studies and genetic experiments identify this factor as a new zinc finger DNA-binding protein which binds GC-rich sequences and contains a domain probably functioning as a transcriptional activator. The new human protein identified in this study was therefore named GC-box-binding zinc finger protein).

L10 ANSWER 16 OF 20 MEDLINE on STN
ACCESSION NUMBER: 97269044 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9111044
TITLE: Characterization of the human thrombopoietin gene promoter. A possible role of an Ets transcription factor, E4TF1/GABP.
AUTHOR: Kamura T; Handa H; Hamasaki N; Kitajima S
CORPORATE SOURCE: Department of Clinical Chemistry and Laboratory Medicine, Kyushu University, Faculty of Medicine, Fukuoka 812-82, Japan.
SOURCE: The Journal of biological chemistry, (1997 Apr 25) Vol. 272, No. 17, pp. 11361-8. Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB000528
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 2 Jun 1997
Last Updated on STN: 3 Mar 2000
Entered Medline: 21 May 1997

AB Thrombopoietin (TPO), the ligand for c-Mpl, is a cytokine that regulates megakaryocyte growth and development. We have cloned the 5'-flanking region of the human TPO gene and analyzed its promoter activity. The human TPO gene promoter lacks a TATA box and directs transcription initiation at multiple sites over a 50-nucleotide region. Transient expression in a human liver cell line (PLC) of promoter fragment-luciferase reporter gene constructs containing a series of 5'-truncated sequences or site-directed mutations identified a sequence 5'-ACTTCCG-3' from -69 to -63 as a positive cis-acting element for high level expression of TPO gene. This sequence contains a core motif (C/A)GGA(A/T) for Ets family proteins in the noncoding strand. Gel mobility shift assays performed with nuclear protein from PLC cells identified a DNA binding protein(s) specific for the element. Anti-E4TF1-60(GABPalpha) or anti-E4TF1-53/47(GABPbeta) antibodies supershifted the complex in gel shift assay. Furthermore, co-expression of E4TF1-60 and E4TF1-53/47 squelched TPO gene expression in PLC and HepG2 cells. It is concluded that Ets family transcription factor E4TF1(GABPalpha/beta), an ubiquitously expressed protein, is required for high level expression of the TPO gene in liver.

L10 ANSWER 17 OF 20 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 1996-105852 [11] WPIDS
CROSS REFERENCE: 1997-512733; 2000-072059
DOC. NO. CPI: C1996-033511 [11]
DOC. NO. NON-CPI: N1996-088666 [11]
TITLE: Interaction trap systems using conformationally-constrained proteins - useful for detection of protein interactions and for identification and isolation of interacting proteins
DERWENT CLASS: B04; D16; S03
INVENTOR: BRENT R; JESSEN T H; MCCOY J M; XU C; XU C W
PATENT ASSIGNEE: (GEHO-C) GEN HOSPITAL CORP; (GEMY-C) GENETICS INST INC; (GEMY-C) GENETICS INST LLC
COUNTRY COUNT: 17

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 9602561	A1	19960201	(199611)*	EN	73[6]	
EP 773952	A1	19970521	(199725)	EN	[0]	
JP 10504713	W	19980512	(199829)	JA	65	
US 6242183	B1	20010605	(200133)	EN		
EP 773952	B1	20031112	(200380)	EN		
DE 69532127	E	20031218	(200407)	DE		
EP 1405911	A1	20040407	(200425)	EN		
ES 2210306	T3	20040701	(200444)	ES		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9602561 A1		WO 1995-US9307	19950720
US 6242183 B1	Cont of	US 1994-278082	19940720

DE 69532127 E	DE 1995-69532127 19950720
EP 773952 A1	EP 1995-928118 19950720
EP 773952 B1	EP 1995-928118 19950720
DE 69532127 E	EP 1995-928118 19950720
EP 1405911 A1 Div Ex	EP 1995-928118 19950720
ES 2210306 T3	EP 1995-928118 19950720
EP 773952 A1	WO 1995-US9307 19950720
JP 10504713 W	WO 1995-US9307 19950720
EP 773952 B1	WO 1995-US9307 19950720
DE 69532127 E	WO 1995-US9307 19950720
JP 10504713 W	JP 1996-505277 19950720
US 6242183 B1	US 1999-249458 19990212
EP 1405911 A1	EP 2003-21647 19950720

FILING DETAILS:

PATENT NO	KIND	PATENT NO
DE 69532127 E	Based on	EP 773952 A
EP 1405911 A1	Div ex	EP 773952 A
ES 2210306 T3	Based on	EP 773952 A
EP 773952 A1	Based on	WO 9602561 A
JP 10504713 W	Based on	WO 9602561 A
EP 773952 B1	Based on	WO 9602561 A
DE 69532127 E	Based on	WO 9602561 A

PRIORITY APPLN. INFO: US 1994-278082 19940720
US 1999-249458 19990212

AN 1996-105852 [11] WPIDS

CR 1997-512733; 2000-072059

AB WO 1996002561 A1 UPAB: 20050702

Determining whether a 1st protein (A) is capable of physically interacting with a 2nd protein (B) comprises providing a host cell which contains: (i) a reporter gene operably linked to a DNA-binding-protein recognition site; (ii) a 1st fusion gene which expresses (A), comprising a 1st protein covalently bonded to a binding moiety which is capable of specifically binding to the DNA-binding-protein recognition site; and (iii) a 2nd fusion gene which expresses (B), comprising a 2nd protein covalently bonded to a gene activating moiety and being conformationally-constrained, and measuring expression of the reporter gene as a measure of an interaction between (A) and (B). The same system is applied in: (i) detecting an interacting protein in a population of proteins; (ii) identifying a candidate interactor; and (iii) assaying an interaction between (A) and (B).

USE - The new method provides an interaction trap system for the identification and analysis of conformationally-constrained proteins, that either physically interact with a 2nd protein of interest or that antagonise or agonise such an interaction.

ADVANTAGE - The system provides rapid and inexpensive methods, having very general utility for identifying and purifying genes encoding a wide range of useful proteins based on the protein's physical interaction with a 2nd polypeptide.

Member(0003)

ABEQ JP 10504713 W UPAB 20050702

Determining whether a 1st protein (A) is capable of physically interacting with a 2nd protein (B) comprises providing a host cell which contains: (i) a reporter gene operably linked to a DNA-binding-protein recognition site; (ii) a 1st fusion gene which expresses (A), comprising a 1st protein covalently bonded to a binding moiety which is capable of specifically

binding to the DNA-binding-protein recognition site; and (iii) a 2nd fusion gene which expresses (B), comprising a 2nd protein covalently bonded to a gene activating moiety and being conformationally-constrained, and measuring expression of the reporter gene as a measure of an interaction between (A) and (B). The same system is applied in: (i) detecting an interacting protein in a population of proteins; (ii) identifying a candidate interactor; and (iii) assaying an interaction between (A) and (B).

USE - The new method provides an interaction trap system for the identification and analysis of conformationally-constrained proteins, that either physically interact with a 2nd protein of interest or that antagonise or agonise such an interaction.

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Member(0004)
ABEQ US 6242183 B1 UPAB 20050702

Determining whether a 1st protein (A) is capable of physically interacting with a 2nd protein (B) comprises providing a host cell which contains: (i) a reporter gene operably linked to a DNA-binding-protein recognition site; (ii) a 1st fusion gene which expresses (A), comprising a 1st protein covalently bonded to a binding moiety which is capable of specifically binding to the DNA-binding-protein recognition site; and (iii) a 2nd fusion gene which expresses (B), comprising a 2nd protein covalently bonded to a gene activating moiety and being conformationally-constrained, and measuring expression of the reporter gene as a measure of an interaction between (A) and (B). The same system is applied in: (i) detecting an interacting protein in a population of proteins; (ii) identifying a candidate interactor; and (iii) assaying an interaction between (A) and (B).

USE - The new method provides an interaction trap system for the identification and analysis of conformationally-constrained proteins, that either physically interact with a 2nd protein of interest or that antagonise or agonise such an interaction.

ADVANTAGE - The system provides rapid and inexpensive methods, having very general utility for identifying and purifying genes encoding a wide range of useful proteins based on the protein's physical interaction with a 2nd polypeptide.

L10 ANSWER 18 OF 20 MEDLINE on STN

ACCESSION NUMBER:	96096536 MEDLINE
DOCUMENT NUMBER:	PubMed ID: 8522191
TITLE:	The upstream region of the SP-B gene: intrinsic promoter activity and glucocorticoid responsiveness related to a new DNA-binding protein.
AUTHOR:	Luzi P; Anceschi M; Strayer D S
CORPORATE SOURCE:	Department of Pathology, Anatomy and Cell Biology, Jefferson Medical College, Philadelphia, PA 19107, USA.
CONTRACT NUMBER:	FD-R-000892 (FDA)
SOURCE:	Gene, (1995 Nov 20) Vol. 165, No. 2, pp. 285-90. Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY:	Netherlands
DOCUMENT TYPE:	Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:	English
FILE SEGMENT:	Priority Journals
OTHER SOURCE:	GENBANK-S80649
ENTRY MONTH:	199601
ENTRY DATE:	Entered STN: 19 Feb 1996 Last Updated on STN: 19 Feb 1996

Entered Medline: 22 Jan 1996

AB We identified and cloned the rabbit SP-B gene, encoding the pulmonary surfactant-associated protein, and sequenced its upstream region from -2635 to +428, including a much larger fragment of the upstream region than has previously been reported for an SP-B for any species. Rabbit SP-B showed substantial homology to its human counterpart in the coding and noncoding regions immediately upstream from the TATAA box. Using a luciferase (Luc) reporter gene (luc) construct we measured promoter activity with a 212-bp fragment (SPB212) from nucleotides (nt) -41 to -252, inclusive. SPB212 functioned as an active promoter in this assay. Further, we identified, cloned and sequenced the cDNA encoding a unique DNA-binding protein, N, that bound SPB212 at approx. -195. When the N cDNA was cloned into the expression vector pKC4 and cotransfected with the luc reporter construct, N significantly enhanced Luc production, but only in the presence of dexamethasone. Therefore, we identified and sequenced a functional promoter region upstream from rabbit SP-B, and isolated and characterized a DNA-binding protein that confers enhanced glucocorticoid responsiveness on this promoter.

L10 ANSWER 19 OF 20 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1994:502505 CAPLUS
DOCUMENT NUMBER: 121:102505
TITLE: Screening for subunits of heterodimeric proteins and the genes encoding them
INVENTOR(S): Kingston, Robert E.; Bunker, Christopher Alden
PATENT ASSIGNEE(S): General Hospital Corp., USA
SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9409133	A1	19940428	WO 1993-US9634	19931006
W: AU, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5322801	A	19940621	US 1992-960981	19921014
AU 9453255	A	19940509	AU 1994-53255	19931006
EP 665884	A1	19950809	EP 1993-923325	19931006
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 11503301	T	19990326	JP 1993-510148	19931006
PRIORITY APPLN. INFO.:			US 1992-960981	A 19921014
			US 1990-510254	B1 19900419
			US 1992-915745	B2 19920107
			US 1992-815880	B1 19920721
			WO 1993-US9634	W 19931006

AB A rapid, simple and inexpensive method to screen and classify proteins as partners of dimeric proteins is described. The method uses fusion proteins of a DNA binding domain and complementary dimerization domains from a candidate protein. Heterodimer formation is detected by the ability of the protein partner to disrupt formation of DNA binding domain homodimers, and so affect the expression of a gene regulated by a homodimeric DNA binding domain in a bacterial host. The method may also be used to identify compds. that inhibit heterodimer formation, and especially to identify compds. which prevent heterodimer formation and activation of oncogenic transcriptional regulatory proteins. Chimeric genes for fusion proteins of cI repressor and the c-myc basic helix-loop-helix domain, optionally including the leucine zipper domain

were prepared and expressed in Escherichia coli. Expression of the chimeric gene increased resistance of the host to infection by λ with inocula of 105-107 required to form clear plaques in spot infection assays. A lacZ gene under control of the PL promoter was repressed by this protein. The dot assay produced a number of false positives when the chimeric gene was resident in the host before infection with a λgt11 cDNA bank; transformation of the bank with the plasmid lowered the number of false positives. The lacZ reporter system also produced false positives; this appears to have been due to instability and plasmid copy number and titration effects.

L10 ANSWER 20 OF 20 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1993:141130 CAPLUS
DOCUMENT NUMBER: 118:141130
TITLE: Characterization of the Trichoderma reesei cbh2 promoter
AUTHOR(S): Stangl, Herbert; Gruber, Franz; Kubicek, Christian P.
CORPORATE SOURCE: Inst. Biochem. Technol. Mikrobiol., TU Wien, Vienna, A-1060, Austria
SOURCE: Current Genetics (1993), 23(2), 115-22
CODEN: CUGED5; ISSN: 0172-8083
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A 613-bp fragment of the 5' upstream region of the T. reesei cbh2 gene (coding for the cellulolytic enzyme cellobiohydrolase II) has been isolated and sequenced. Fusion of this fragment to the E. coli uidA gene (coding for β-glucuronidase) leads to, albeit low, expression of β-glucuronidase activity in the presence of cellulose and upon the addition of low mol. weight inducers (sophorose, lactose) of cellobiohydrolase II. It also governed the formation of β-glucuronidase activity during sporulation and its transport to the conidial surface. However, despite the presence of a signal peptide in the cbh2:uidA fusion, β-glucuronidase was not secreted in T. reesei. Defined fragments of the 613-bp promoter region were isolated and used to identify areas involved in the regulation of cbh2 expression by protein-DNA binding assays.
At least two binding areas, between -443/-363 and -363/-173, resp., were identified. In both areas, the DNA-protein complex observed was appreciably larger when cell-free exts. from sophorose-induced mycelia were used. This suggests that at least one of the proteins regulating cbh2 transcription is itself induced by cellulose.

```
=> e joung j?/au
E1          12     JOUNG J W/AU
E2          19     JOUNG J Y/AU
E3           0 --> JOUNG J?/AU
E4           2     JOUNG JAE HEE/AU
E5           1     JOUNG JAE JOUNG/AU
E6           1     JOUNG JAE KEITH/AU
E7           3     JOUNG JAE WOO/AU
E8           1     JOUNG JAE YEOL/AU
E9           7     JOUNG JAE YOUL/AU
E10          4     JOUNG JAE YOUNG/AU
E11          1     JOUNG JAERUYL/AU
E12          4     JOUNG JAEWOO/AU

=> e joung j k?/au
E1          12     JOUNG J J/AU
E2          37     JOUNG J K/AU
E3           0 --> JOUNG J K?/AU
E4          40     JOUNG J KEITH/AU
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E5          16     JOUNG J M/AU
E6           3     JOUNG J O/AU
E7           8     JOUNG J S/AU
E8          12     JOUNG J W/AU
E9          19     JOUNG J Y/AU
E10          2     JOUNG JAE HEE/AU
E11          1     JOUNG JAE JOUNG/AU
E12          1     JOUNG JAE KEITH/AU

=> e2 or e4
L11         77 "JOUNG J K"/AU OR "JOUNG J KEITH"/AU

=> DNA and l11
L12         57 DNA AND L11

=> dup rem l12
PROCESSING COMPLETED FOR L12
L13          25 DUP REM L12 (32 DUPLICATES REMOVED)

=> dup rem l11
PROCESSING COMPLETED FOR L11
L14          30 DUP REM L11 (47 DUPLICATES REMOVED)

=> t ti l14 1-30

L14  ANSWER 1 OF 30  WPIDS COPYRIGHT 2007       THE THOMSON CORP on STN

TI   System and method for linking cooperated service welfare expense
     information with user information in real-time

L14  ANSWER 2 OF 30     MEDLINE on STN
TI   Synthetic protein-protein interaction domains created by shuffling
     Cys2His2 zinc-fingers.

L14  ANSWER 3 OF 30  EMBASE  COPYRIGHT (c) 2007 Elsevier B.V. All rights
     reserved on STN
TI   Synthetic protein-protein interaction domains created by shuffling Cys
     (2)His(2) zinc-fingers.

L14  ANSWER 4 OF 30     MEDLINE on STN                  DUPLICATE 1
TI   Counter-selectable marker for bacterial-based interaction trap systems.

L14  ANSWER 5 OF 30  CAPLUS  COPYRIGHT 2007 ACS on STN
TI   Synthetic protein-protein interaction domains created by shuffling
     Cys2His2 zinc-fingers

L14  ANSWER 6 OF 30  WPIDS COPYRIGHT 2007       THE THOMSON CORP on STN

TI   Determining interaction of a test nucleic acid molecule with a test
     polypeptide, by introducing reporter vectors from first cell population in
     selective condition into second population in counterselective conditions,
     measuring cell growth

L14  ANSWER 7 OF 30     MEDLINE on STN                  DUPLICATE 2
TI   Repression of phase-variable cup gene expression by H-NS-like proteins in
     Pseudomonas aeruginosa.

L14  ANSWER 8 OF 30     MEDLINE on STN                  DUPLICATE 3
TI   A combined yeast/bacteria two-hybrid system: development and evaluation.

L14  ANSWER 9 OF 30  CAPLUS  COPYRIGHT 2007 ACS on STN
TI   Bacterial two-hybrid system for studying and modifying protein-protein
```

interactions

L14 ANSWER 10 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
TI Counter-selectable marker for bacterial-based interaction trap systems

L14 ANSWER 11 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 4
TI Methods for isolating NRSF-based non-natural multi-zinc finger (Zf) proteins that bind to an extended target DNA sequence of interest

L14 ANSWER 12 OF 30 MEDLINE on STN DUPLICATE 5
TI Allosteric inhibition of zinc-finger binding in the major groove of DNA by minor-groove binding ligands.

L14 ANSWER 13 OF 30 MEDLINE on STN DUPLICATE 6
TI High-throughput beta-galactosidase assay for bacterial cell-based reporter systems.

L14 ANSWER 14 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
TI High-throughput β-galactosidase assay for bacterial cell-based reporter systems

L14 ANSWER 15 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 7
TI Engineered Cys2His2 zinc finger DNA-binding domains

L14 ANSWER 16 OF 30 MEDLINE on STN DUPLICATE 8
TI Highly specific zinc finger proteins obtained by directed domain shuffling and cell-based selection.

L14 ANSWER 17 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
TI Methods and compositions for interaction trap assays

L14 ANSWER 18 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
TI Yeast and bacterial two-hybrid selection systems for studying protein-protein interactions

L14 ANSWER 19 OF 30 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
TI Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system.

L14 ANSWER 20 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 9
TI Interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions

L14 ANSWER 21 OF 30 MEDLINE on STN DUPLICATE 10
TI Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system.

L14 ANSWER 22 OF 30 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system

L14 ANSWER 23 OF 30 MEDLINE on STN DUPLICATE 11
TI A bacterial two-hybrid selection system for studying protein-DNA and protein-protein interactions.

L14 ANSWER 24 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
TI Interaction trap assay and its reagents

L14 ANSWER 25 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 12
TI An interaction trap assay system using the λ repressor for use in a

bacterial host

L14 ANSWER 26 OF 30 MEDLINE on STN DUPLICATE 13
TI Activation of prokaryotic transcription through arbitrary protein-protein contacts.

L14 ANSWER 27 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
TI Synergistic activation of transcription in E. coli

L14 ANSWER 28 OF 30 MEDLINE on STN DUPLICATE 14
TI Genetic strategy for analyzing specificity of dimer formation: Escherichia coli cyclic AMP receptor protein mutant altered in its dimerization specificity.

L14 ANSWER 29 OF 30 MEDLINE on STN DUPLICATE 15
TI Synergistic activation of transcription by bacteriophage lambda cI protein and E. coli cAMP receptor protein.

L14 ANSWER 30 OF 30 MEDLINE on STN DUPLICATE 16
TI Synergistic activation of transcription by Escherichia coli cAMP receptor protein.

=> d ibib abs l14 1-30

L14 ANSWER 1 OF 30 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2006-705007 [73] WPIDS
TITLE: System and method for linking cooperated service welfare expense information with user information in real-time
DERWENT CLASS: T01
INVENTOR: JOUNG J K
PATENT ASSIGNEE: (EXAN-N) EXANADU CORP
COUNTRY COUNT: 1

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
KR 2006015354	A	20060216	(200673)*	KO	[1]	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
KR 2006015354	A	KR 2006-10298	20060202

PRIORITY APPLN. INFO: KR 2006-10298 20060202
AN 2006-705007 [73] WPIDS
AB KR 2006015354 A UPAB: 20061113
NOVELTY - A system and a method for linking cooperated service welfare expense information with user information in real-time are provided to settle a welfare expense by linking with a welfare expense policy of each member customer and automatically offset the settled welfare expense.
DETAILED DESCRIPTION - A user (400) receives selective welfare services in the online. Each cooperated company server (300) provides cooperated welfare services to users connected through the online. A real-time cooperated service welfare expense linking server (200) fixes the welfare expense policy of each member company, settles the welfare expense by linking personal information of the connected user with the welfare expense information in real-time, and automatically offsets the settled welfare expense. A customer company manager computer (100) manages the cooperated service welfare expense of each customer company by

connecting to the real-time cooperated service welfare expense linking server.

L14 ANSWER 2 OF 30 MEDLINE on STN
ACCESSION NUMBER: 2006304179 MEDLINE
DOCUMENT NUMBER: PubMed ID: 16732192
TITLE: Synthetic protein-protein interaction domains created by shuffling Cys2His2 zinc-fingers.
AUTHOR: Giesecke Astrid V; Fang Rui; Joung J Keith
CORPORATE SOURCE: Molecular Pathology Unit, Department of Pathology, Massachusetts General Hospital, Charlestown, MA 02129, USA.
CONTRACT NUMBER: K08 DK002883 (NIDDK)
R01 GM069906 (NIGMS)
R01 GM072621 (NIGMS)
SOURCE: Molecular systems biology [electronic resource], (2006) Vol. 2, pp. 2006.2011. Electronic Publication: 2006-03-21. Journal code: 101235389. E-ISSN: 1744-4292.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200608
ENTRY DATE: Entered STN: 31 May 2006
Last Updated on STN: 5 Aug 2006
Entered Medline: 4 Aug 2006
AB Cys2His2 zinc-fingers (C2H2 ZFs) mediate a wide variety of protein-DNA and protein-protein interactions. DNA-binding C2H2 ZFs can be shuffled to yield artificial proteins with different DNA binding specificities. Here we demonstrate that shuffling of C2H2 ZFs from transcription factor dimerization zinc-finger (DZF) domains can also yield two-finger DZFs with novel protein-protein interaction specificities. We show that these synthetic protein-protein interaction domains can be used to mediate activation of a single-copy reporter gene in bacterial cells and of an endogenous gene in human cells. In addition, the synthetic two-finger domains we constructed can also be linked together to create more extended, four-finger interfaces. Our results demonstrate that shuffling of C2H2 ZFs can yield artificial protein-interaction components that should be useful for applications in synthetic biology.

L14 ANSWER 3 OF 30 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
ACCESSION NUMBER: 2006303704 EMBASE
TITLE: Synthetic protein-protein interaction domains created by shuffling Cys (2)His(2) zinc-fingers.
AUTHOR: Giesecke A.V.; Fang R.; Joung J.K.
CORPORATE SOURCE: J.K. Joung, Molecular Pathology Unit, Department of Pathology, Massachusetts General Hospital, 149 13th Street, Charlestown, MA 02129, United States. jjoung@partners.org
SOURCE: Molecular Systems Biology, (16 May 2006) Vol. 2, pp. 2006.0011. arn. msb4100053.
Refs: 53
ISSN: 1744-4292 E-ISSN: 1744-4292
PUBLISHER IDENT.: M4100053
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 21 Jul 2006
Last Updated on STN: 21 Jul 2006
AB Cys(2)His(2) zinc-fingers (C2H2 ZFs) mediate a wide variety of protein-DNA

and protein-protein interactions. DNA-binding C2H2 ZFs can be shuffled to yield artificial proteins with different DNA-binding specificities. Here we demonstrate that shuffling of C2H2 ZFs from transcription factor dimerization zinc-finger (DZF) domains can also yield two-finger DZFs with novel protein-protein interaction specificities. We show that these synthetic protein-protein interaction domains can be used to mediate activation of a single-copy reporter gene in bacterial cells and of an endogenous gene in human cells. In addition, the synthetic two-finger domains we constructed can also be linked together to create more extended, four-finger interfaces. Our results demonstrate that shuffling of C2H2 ZFs can yield artificial protein-interaction components that should be useful for applications in synthetic biology. .COPYRGT. 2006 EMBO and Nature Publishing Group.

L14 ANSWER 4 OF 30 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2006138723 MEDLINE
DOCUMENT NUMBER: PubMed ID: 16526407
TITLE: Counter-selectable marker for bacterial-based interaction trap systems.
AUTHOR: Meng Xiangdong; Smith Robin M; Giesecke Astrid V; Joung J Keith; Wolfe Scot A
CORPORATE SOURCE: University of Massachusetts Medical School, Worcester, MA 01605, USA.
CONTRACT NUMBER: R01GM068110 (NIGMS)
R01GM072621 (NIGMS)
R01GN969906
SOURCE: BioTechniques, (2006 Feb) Vol. 40, No. 2, pp. 179-84.
Journal code: 8306785. ISSN: 0736-6205.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200604
ENTRY DATE: Entered STN: 11 Mar 2006
Last Updated on STN: 7 Apr 2006
Entered Medline: 6 Apr 2006

AB Counter-selectable markers can be used in two-hybrid systems to search libraries for a protein or compound that interferes with a macromolecular interaction or to identify macromolecules from a population that cannot mediate a particular interaction. In this report, we describe the adaptation of the yeast URA3/5-FOA counter-selection system for use in bacterial interaction trap experiments. Two different URA3 reporter systems were developed that allow robust counter-selection: (i) a single copy F' episome reporter and (ii) a co-cistronic HIS3-URA3 reporter vector. The HIS3-URA3 reporter can be used for either positive or negative selections in appropriate bacterial strains. These reagents extend the utility of the bacterial two-hybrid system as an alternative to its yeast-based counterpart.

L14 ANSWER 5 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2006:384193 CAPLUS
DOCUMENT NUMBER: 145:182549
TITLE: Synthetic protein-protein interaction domains created by shuffling Cys2His2 zinc-fingers
AUTHOR(S): Giesecke, Astrid V.; Fang, Rui; Joung, J. Keith
CORPORATE SOURCE: Molecular Pathology Unit, Department of Pathology, Massachusetts General Hospital, Charlestown, MA, USA
SOURCE: Molecular Systems Biology (2006) No pp. given
CODEN: MSBOC3; ISSN: 1744-4292
URL: http://www.nature.com/msb/journal/v2/n1/pdf/msb4100053.pdf

PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English
AB. Cys2His2 zinc-fingers (C2H2 ZFs) mediate a wide variety of protein-DNA and protein-protein interactions. DNA-binding C2H2 ZFs can be shuffled to yield artificial proteins with different DNA-binding specificities. Here we demonstrate that shuffling of C2H2 ZFs from transcription factor dimerization zinc-finger (DZF) domains can also yield two-finger DZFs with novel protein-protein interaction specificities. We show that these synthetic protein-protein interaction domains can be used to mediate activation of a single-copy reporter gene in bacterial cells and of an endogenous gene in human cells. In addition, the synthetic two-finger domains we constructed can also be linked together to create more extended, four-finger interfaces. Our results demonstrate that shuffling of C2H2 ZFs can yield artificial protein-interaction components that should be useful for applications in synthetic biol.
REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 6 OF 30 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2006-056007 [06] WPIDS
DOC. NO. CPI: C2006-020937 [06]
TITLE: Determining interaction of a test nucleic acid molecule with a test polypeptide, by introducing reporter vectors from first cell population in selective condition into second population in counterselective conditions, measuring cell growth
DERWENT CLASS: B04; D16
INVENTOR: JOUNG J K; MENG X; WOLFE S A
PATENT ASSIGNEE: (JOUN-I) JOUNG J K; (MENG-I) MENG X; (WOLF-I) WOLFE S A
COUNTRY COUNT: 1

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
US 20050287550	A1	20051229	(200606)*	EN	52[16]	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 20050287550	A1 Provisional	US 2004-541464P	20040202
US 20050287550	A1	US 2005-50174	20050202

PRIORITY APPLN. INFO: US 2005-50174 20050202
US 2004-541464P 20040202
AN 2006-056007 [06] WPIDS
AB US 20050287550 A1 UPAB: 20060124
NOVELTY - Determining interaction of test nucleic acid with test polypeptide, by maintaining first population of host cells having reporter vector that has selectable and counterselectable reporter genes; chimeric gene, under selective conditions, introducing the isolated vectors into second population of host lacking chimeric gene and maintaining under counterselective conditions that inhibit cell growth, measuring growth of second population of host.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:
(1) a vector (V1) comprising a selectable reporter gene and counterselectable reporter gene, where the selectable reporter gene and counterselectable reporter gene are operably linked to a promoter, and DNA sequence insertion site upstream of the promoter, where the DNA sequence insertion site is positioned to enable binding of a DNA binding domain to

the DNA sequence to drive expression of the reporter genes;

(2) a library (I) comprising several prokaryotic cells or colonies of prokaryotic cells, where each cell comprises reporter vector having a selectable reporter gene, counterselectable reporter gene, and DNA molecule, where the selectable reporter gene and counterselectable reporter gene are operably linked to the DNA molecule, and where each cell or each colony of cells comprises different DNA molecule;

(3) a kit (K1) comprising (I) and a vector for encoding a fusion protein, where the vector comprises transcriptional and translational elements that direct expression of the fusion protein in a prokaryotic host cell, DNA sequence that encodes a gene activation domain that is functionally associated with the transcriptional and translational elements of the vector, and one or more sites for inserting a DNA sequence encoding a test polypeptide into the vector in such a manner that the test polypeptide is expressed in frame as part of the fusion protein containing the gene activation domain;

(4) determining (M2) whether a first test polypeptide does or does not interact with a second test polypeptide, involves providing a prokaryotic host cell that comprises counterselectable reporter gene operably linked to a transcriptional regulatory sequence that includes a DNA binding site for a DNA binding domain, first chimeric gene that encodes a first fusion protein, which comprises the first test polypeptide fused to the DNA binding domain, and a second chimeric gene that encodes a second fusion protein, which comprises the second test polypeptide fused to a gene activating domain, where interaction of the first test polypeptide and the second test polypeptide in the host cell results in an increase in expression of the reporter gene, providing a control prokaryotic host cell that comprises counterselectable reporter gene operably linked to a transcriptional regulatory sequence that includes a DNA binding site for a DNA binding domain, and optionally the first chimeric gene or the second chimeric gene, but not both, growing the host cell and control host cell under counterselective conditions, and measuring growth of the host cell, where a decrease in growth as compared to the growth of a control host cell indicates an interaction of the first test polypeptide and the second test polypeptide and no change in growth indicates no interaction of the first test polypeptides and the second test polypeptides; and

(5) a prokaryotic cell (II) comprising an exogenous counterselectable reporter gene that is operably linked to a promoter having a DNA binding recognition site, where the prokaryotic cell lacks a functional gene that is homologous to the exogenous counterselectable reporter gene.

USE - (M1) is useful for determining whether test nucleic acid molecule interacts with test polypeptide (claimed).

ADVANTAGE - (M1) provides a high-throughput assay for determining the sequence specificity of the DNA binding protein e.g transcriptional factor.

L14 ANSWER 7 OF 30 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 2005414099 MEDLINE
DOCUMENT NUMBER: PubMed ID: 16043713
TITLE: Repression of phase-variable cup gene expression by H-NS-like proteins in Pseudomonas aeruginosa.
AUTHOR: Vallet-Gely Isabelle; Donovan Katherine E; Fang Rui; Joung J Keith; Dove Simon L
CORPORATE SOURCE: Division of Infectious Diseases, Children's Hospital, Harvard Medical School, Boston, MA 02115, USA.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2005 Aug 2) Vol. 102, No. 31, pp. 11082-7. Electronic Publication: 2005-07-25. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200509
ENTRY DATE: Entered STN: 4 Aug 2005
Last Updated on STN: 21 Sep 2005
Entered Medline: 20 Sep 2005

AB The cupA gene cluster of Pseudomonas aeruginosa encodes components of a putative fimbrial structure that enable this opportunistic human pathogen to form biofilms on abiotic surfaces. In P. aeruginosa, cupA gene expression is repressed by MvaT, a putative transcription regulator thought to belong to the H-NS family of nucleoid-associated proteins that typically function by repressing transcription. Here, we present evidence that MvaT controls phase-variable (ON/OFF) expression of the cupA fimbrial gene cluster. Using a directed proteomic approach, we show that MvaT associates with a related protein in P. aeruginosa called MvaU. Analysis with a bacterial two-hybrid system designed to facilitate the study of protein dimerization indicates that MvaT and MvaU can form both heteromeric and homomeric complexes, and that formation of these complexes is mediated through the N-terminal regions of MvaT and MvaU, both of which are predicted to adopt a coiled-coil conformation. We show further that, like MvaT, MvaU can repress phase-variable expression of the cupA gene cluster. Our findings suggest that fimbrial genes important for biofilm formation can be expressed in a phase-variable manner in P. aeruginosa, provide insight into the molecular mechanism of MvaT-dependent gene control, and lend further weight to the postulate that MvaT proteins are H-NS-like in nature.

L14 ANSWER 8 OF 30 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 2005296407 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15781424
TITLE: A combined yeast/bacteria two-hybrid system: development and evaluation.
AUTHOR: Serebriiskii Ilya G; Fang Rui; Latypova Ekaterina; Hopkins Richard; Vinson Charles; Joung J Keith; Golemis Erica A
CORPORATE SOURCE: Division of Basic Science, Fox Chase Cancer Center, Philadelphia, Pennsylvania 19111, USA..
ig_serebriiskii@fccc.edu
CONTRACT NUMBER: CA06927 (NCI)
K08-DK02883 (NIDDK)
R01-CA63366 (NCI)
R01-GM069906 (NIGMS)
SOURCE: Molecular & cellular proteomics : MCP, (2005 Jun) Vol. 4, No. 6, pp. 819-26. Electronic Publication: 2005-03-20.
Journal code: 101125647. ISSN: 1535-9476.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200509
ENTRY DATE: Entered STN: 9 Jun 2005
Last Updated on STN: 21 Sep 2005
Entered Medline: 20 Sep 2005

AB Two-hybrid screening is a standard method used to identify and characterize protein-protein interactions and has become an integral component of many proteomic investigations. The two-hybrid system was initially developed using yeast as a host organism. However, bacterial two-hybrid systems have also become common laboratory tools and are preferred in some circumstances, although yeast and bacterial two-hybrid systems have never been directly compared. We describe here the development of a unified yeast and bacterial two-hybrid system in which a

single bait expression plasmid is used in both organismal milieus. We use a series of leucine zipper fusion proteins of known affinities to compare interaction detection using both systems. Although both two-hybrid systems detected interactions within a comparable range of interaction affinities, each demonstrated unique advantages. The yeast system produced quantitative readout over a greater dynamic range than that observed with bacteria. However, the phenomenon of "autoactivation" by baits was less of a problem in the bacterial system than in the yeast. Both systems identified physiological interactors for a library screen with a cI-Ras test bait; however, non-identical interactors were obtained in yeast and bacterial screens. The ability to rapidly shift between yeast and bacterial systems provided by these new reagents should provide a marked advantage for two-hybrid investigations. In addition, the modified expression vectors we describe in this report should be useful for any application requiring facile expression of a protein of interest in both yeast and bacteria.

L14 ANSWER 9 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2005:1252351 CAPLUS
DOCUMENT NUMBER: 145:181393
TITLE: Bacterial two-hybrid system for studying and modifying protein-protein interactions
AUTHOR(S): Giesecke, Astrid V.; Joung, J. Keith
CORPORATE SOURCE: Molecular Pathology Unit & Center for Cancer Research, Massachusetts General Hospital, Charlestown, MA, 02129, USA
SOURCE: Protein-Protein Interactions (2nd Edition) (2005), 195-216. Editor(s): Golemis, Erica A.; Adams, Peter D. Cold Spring Harbor Laboratory Press: Cold Spring Harbor, N. Y.
CODEN: 69HQCK; ISBN: 0-87969-723-7
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The bacterial two-hybrid system is based on the observation that any sufficiently strong protein-protein interaction can mediate transcriptional activation of a weak promoter in E. coli. Other applications of bacterial two-hybrid systems are as a reporter method for mutational anal., a selection method for reengineering protein function, and as a selection method for identifying interaction partners from cDNA libraries. Protocols for these applications for bacterial two-hybrid system involve four stages. First is the construction of a selection strain harboring a potentially suppressible mutation in protein Y followed by a construction of a library of DBD-X variants. Third stage involves the introduction of the library into selection-strain cells and performance of selection. Lastly, potential pos. candidates are confirmed and sequenced.
REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 10 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2006:151476 CAPLUS
DOCUMENT NUMBER: 144:481913
TITLE: Counter-selectable marker for bacterial-based interaction trap systems
AUTHOR(S): Meng, Xiangdong; Smith, Robin M.; Giesecke, Astrid V.; Joung, J. Keith; Wolfe, Scot A.
CORPORATE SOURCE: University of Massachusetts Medical School, Worcester, MA, USA
SOURCE: BioTechniques (2005), Volume Date 2006, 40(2), 179-184
CODEN: BTNQDO; ISSN: 0736-6205
PUBLISHER: Informa Life Sciences Publishing
DOCUMENT TYPE: Journal

LANGUAGE: English

AB Counter-selectable markers can be used in two-hybrid systems to search libraries for a protein or compound that interferes with a macromol. interaction or to identify macromols. from a population that cannot mediate a particular interaction. In this report, the authors describe the adaptation of the yeast URA3/5-FOA counter-selection system for use in bacterial interaction trap expts. Two different URA3 reporter systems were developed that allow robust counter-selection: (i) a single copy F' episome reporter and (ii) a co-cistronic HIS3-URA3 reporter vector. The HIS3-URA3 reporter can be used for either pos. or neg. selections in appropriate bacterial strains. These reagents extend the utility of the bacterial two-hybrid system as an alternative to its yeast-based counterpart.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 11 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 4

ACCESSION NUMBER: 2004:996299 CAPLUS

DOCUMENT NUMBER: 141:406781

TITLE: Methods for isolating NRSF-based non-natural multi-zinc finger (Zf) proteins that bind to an extended target DNA sequence of interest

INVENTOR(S): Joung, J. Keith

PATENT ASSIGNEE(S): The General Hospital Corporation, USA

SOURCE: PCT Int. Appl., 140 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2004099367	A2	20041118	WO 2003-US34028		20031023
WO 2004099367	A3	20060720			
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW					
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG					
AU 2003304087	A1	20041126	AU 2003-304087		20031023
US 2006246440	A1	20061102	US 2006-532031		20060501
PRIORITY APPLN. INFO.:			US 2002-420458P	P	20021023
			US 2003-466712P	P	20030430
			US 2003-466889P	P	20030430
			US 2003-477314P	P	20030609
			WO 2003-US34028	W	20031023

AB The present invention relates to non-naturally occurring Zinc finger (Zf) proteins that are selected for binding to a DNA sequence of interest. The non-naturally occurring zinc finger proteins of the present invention are based on the sequence of zinc finger proteins having more than three zinc fingers, such as NRSF (neuron-restrictive silencing factor)/REST, and are capable of binding extended DNA target sequences with high affinity and specificity. NRSF binds to a 21 bp DNA sequence called the Neuron Restrictive Silencer Element (NRSE). The present invention provides a method for rapidly selecting multi-finger Zf polypeptides that bind to any desired sequence of interest comprising a target site, termed "context

sensitive parallel optimization" (CSPO). The binding of NRSF to DNA was studied by bacterial two-hybrid system. Targeted re-engineering of NRSF zinc finger variants with altered DNA-binding specificity was demonstrated.

L14 ANSWER 12 OF 30 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 2004156831 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15049695
TITLE: Allosteric inhibition of zinc-finger binding in the major groove of DNA by minor-groove binding ligands.
AUTHOR: Nguyen-Hackley Doan H; Ramm Elizabeth; Taylor Christina M; Joung J Keith; Dervan Peter B; Pabo Carl O
CORPORATE SOURCE: Division of Chemistry and Chemical Engineering, California Institute of Technology, Pasadena, California 91125, USA.
CONTRACT NUMBER: GM 51747 (NIGMS)
SOURCE: Biochemistry, (2004 Apr 6) Vol. 43, No. 13, pp. 3880-90. Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200407
ENTRY DATE: Entered STN: 31 Mar 2004
Last Updated on STN: 30 Jul 2004
Entered Medline: 29 Jul 2004

AB In recent years, two methods have been developed that may eventually allow the targeted regulation of a broad repertoire of genes. The engineered protein strategy involves selecting Cys(2)His(2) zinc finger proteins that will recognize specific sites in the major groove of DNA. The small molecule approach utilizes pairing rules for pyrrole-imidazole polyamides that target specific sites in the minor groove. To understand how these two methods might complement each other, we have begun exploring how polyamides and zinc fingers interact when they bind the same site on opposite grooves of DNA. Although structural comparisons show no obvious source of van der Waals collisions, we have found a significant "negative cooperativity" when the two classes of compounds are directed to the overlapping sites. Examining available crystal structures suggests that this may reflect differences in the precise DNA conformation, especially with regard to width and depth of the grooves, that is preferred for binding. These results may give new insights into the structural requirements for zinc finger and polyamide binding and may eventually lead to the development of even more powerful and flexible schemes for regulating gene expression.

L14 ANSWER 13 OF 30 MEDLINE on STN DUPLICATE 6
ACCESSION NUMBER: 2004145516 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15038156
TITLE: High-throughput beta-galactosidase assay for bacterial cell-based reporter systems.
AUTHOR: Thibodeau Stacey A; Fang Rui; Joung J Keith
CORPORATE SOURCE: Massachusetts General Hospital, Charlestown, MA, USA.
CONTRACT NUMBER: K08DK02883 (NIDDK)
SOURCE: BioTechniques, (2004 Mar) Vol. 36, No. 3, pp. 410-5. Journal code: 8306785. ISSN: 0736-6205.
PUB. COUNTRY: United States
DOCUMENT TYPE: (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200410
ENTRY DATE: Entered STN: 25 Mar 2004

Last Updated on STN: 6 Oct 2004
Entered Medline: 5 Oct 2004

L14 ANSWER 14 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2004:233853 CAPLUS
DOCUMENT NUMBER: 141:290994
TITLE: High-throughput β-galactosidase assay for bacterial cell-based reporter systems
AUTHOR(S): Thibodeau, Stacey A.; Fang, Rui; Joung, J. Keith
CORPORATE SOURCE: Massachusetts General Hospital, Charlestown, MA, 02129, USA
SOURCE: BioTechniques (2004), 36(3), 410,412-415
CODEN: BTNQDO; ISSN: 0736-6205
PUBLISHER: Eaton Publishing Co.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A complete and optimized protocol for growing bacterial cultures and performing kinetic β-galactosidase assays in a 96-well format is described. This new protocol is validated by demonstrating that it yields β-galactosidase values essentially identical to those obtained using the original Miller protocol on matched samples. The increased throughput afforded by this modified assay has already significantly altered the use of β-galactosidase assays in laboratory This high-throughput kinetic protocol is rapid, less labor-intensive than the original Miller method, and expands the possibilities for high-throughput applications requiring large nos. of β-galactosidase assays from bacterial cells.
REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 15 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 7
ACCESSION NUMBER: 2005:59453 CAPLUS
DOCUMENT NUMBER: 142:458621
TITLE: Engineered Cys2His2 zinc finger DNA-binding domains
AUTHOR(S): Hirsh, Andrew S.; Joung, J. Keith
CORPORATE SOURCE: Molecular Pathology Unit, Massachusetts General Hospital, Charlestown, MA, 02129, USA
SOURCE: Gene Therapy and Regulation (2004), 2(3), 191-206
CODEN: GTREBR; ISSN: 1388-9532
PUBLISHER: Brill Academic Publishers
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Gene therapy reagents such as artificial transcription factors and site-specific endonucleases require "made-to-order" DNA-binding domains with high affinity and specificity for novel target sequences. Cys2His2 zinc finger proteins are the best understood and most commonly used framework for design and selection of such domains. Though a number of design strategies have been described in the literature, they vary significantly in their reliability and ease of execution. This situation has made it difficult for the non-specialist researcher to know how best to construct zinc finger proteins for their application of interest. This article reviews the current state of the technol. and its limitations, and discusses prospects for improving our ability to make customized DNA-binding modules.
REFERENCE COUNT: 74 THERE ARE 74 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 16 OF 30 MEDLINE on STN DUPLICATE 8
ACCESSION NUMBER: 2003481808 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14527993
TITLE: Highly specific zinc finger proteins obtained by directed domain shuffling and cell-based selection.

AUTHOR: Hurt Jessica A; Thibodeau Stacey A; Hirsh Andrew S; Pabo Carl O; Joung J Keith
CORPORATE SOURCE: Molecular Pathology Unit, Division of Molecular Pathology and Research, Department of Pathology, Massachusetts General Hospital, Charlestown, MA 02129, USA.
CONTRACT NUMBER: 5T32 CA 09216 (NCI)
K08 DK 02883 (NIDDK)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2003 Oct 14) Vol. 100, No. 21, pp. 12271-6. Electronic Publication: 2003-10-03.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200312
ENTRY DATE: Entered STN: 16 Oct 2003
Last Updated on STN: 19 Dec 2003
Entered Medline: 4 Dec 2003

AB Engineered Cys2His2 zinc finger proteins (ZFPs) can mediate regulation of endogenous gene expression in mammalian cells. Ideally, all zinc fingers in an engineered multifinger protein should be optimized concurrently because cooperative and context-dependent contacts can affect DNA recognition. However, the simultaneous selection of key contacts in even three fingers from fully randomized libraries would require the consideration of >10(24) possible combinations. To address this challenge, we have developed a novel strategy that utilizes directed domain shuffling and rapid cell-based selections. Unlike previously described methods, our strategy is amenable to scale-up and does not sacrifice combinatorial diversity. Using this approach, we have successfully isolated multifinger proteins with improved in vitro and in vivo function. Our results demonstrate that both DNA binding affinity and specificity are important for cellular function and also provide a general approach for optimizing multidomain proteins.

L14 ANSWER 17 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2002:658658 CAPLUS
DOCUMENT NUMBER: 137:197850
TITLE: Methods and compositions for interaction trap assays
INVENTOR(S): Joung, J. Keith; Miller, Jeffrey; Pabo, Carl O.
PATENT ASSIGNEE(S): Massachusetts Institute of Technology, USA
SOURCE: U.S. Pat. Appl. Publ., 61 pp., Cont.-in-part of U.S. Ser. No. 858,852.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2002119498	A1	20020829	US 2001-990762		20011114
US 7029847	B2	20060418			
US 2003044787	A1	20030306	US 2001-858852		20010516
US 2004146931	A1	20040729	US 2004-801994		20040316
US 2005064477	A1	20050324	US 2004-915233		20040810
PRIORITY APPLN. INFO.:			US 2000-204509P	P	20000516
			US 2001-858852	A2	20010516
			US 2001-990762	A3	20011114

AB The invention concerns methods and compns. for interaction trap assays for detecting protein-protein, protein-DNA, or protein-RNA interactions. The

methods and compns. of the invention may also be used to identify agents which may agonize or antagonize a protein-protein, protein-DNA, or protein-RNA interaction. In certain embodiments, the interaction trap system of the invention is useful for screening libraries with greater than 107 members. In other embodiments, the interaction trap system of the invention is used in conjunction with flow cytometry. The invention further provides a means for simultaneously screening a target protein or nucleic acid sequence for the ability to interact with two or more test proteins or nucleic acids.

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 18 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2002:75438 CAPLUS
DOCUMENT NUMBER: 137:226954
TITLE: Yeast and bacterial two-hybrid selection systems for studying protein-protein interactions
AUTHOR(S): Serebriiskii, Ilya; Joung, J. Keith
CORPORATE SOURCE: Fox Chase Cancer Center, Philadelphia, PA, 10111, USA
SOURCE: Protein-Protein Interactions (2002), 93-142. Editor(s): Golemis, Erica. Cold Spring Harbor Laboratory Press: Cold Spring Harbor, N. Y. CODEN: 69CFYI; ISBN: 0-87969-628-1
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review describes the yeast and bacterial two-hybrid systems as powerful methods for analyzing protein-protein interactions. The screening for novel proteins using the interaction trap variant of the yeast two-hybrid system is discussed. The bacterial two-hybrid system is based on the observation that two interacting proteins X and Y can trigger transcriptional activation of a weak promoter in Escherichia coli.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 19 OF 30 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 2002060487 EMBASE
TITLE: Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system.
AUTHOR: Joung J.K.
CORPORATE SOURCE: J.K. Joung, Department of Pathology, Division of Molecular Pathology, Massachusetts General Hospital, 149 13th Street, Charlestown, MA 02129, United States. jjoung@partners.org
SOURCE: Journal of Cellular Biochemistry, (2002) Vol. 84, No. SUPPL. 37, pp. 53-57. .
Refs: 12
ISSN: 0730-2312 CODEN: JCEBD5
COUNTRY: United States
DOCUMENT TYPE: Journal; Conference Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 1 Mar 2002
Last Updated on STN: 1 Mar 2002

AB A bacterial two-hybrid system based on transcriptional activation in E. coli has recently been described. A variety of different protein-DNA and protein-protein interactions from bacteria, yeast, and humans have been studied using this bacterial-based system. The method, because it is based in bacteria, offers significant advantages relative to its yeast counterpart including the ability to analyze complex libraries > 10(8) in size, ease of use, and speed. The ability to easily and rapidly process very large libraries make this system a powerful tool for identifying,

modifying, or optimizing protein-DNA and protein-protein interactions. .COPYRGT. 2002 Wiley-Liss, Inc.

L14 ANSWER 20 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 9
ACCESSION NUMBER: 2001:851433 CAPLUS
DOCUMENT NUMBER: 136:1569
TITLE: Interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions
INVENTOR(S): Joung, J. Keith; Miller, Jeffrey; Pabo, Carl O.
PATENT ASSIGNEE(S): Massachusetts Institute of Technology, USA
SOURCE: PCT Int. Appl., 196 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001088197	A2	20011122	WO 2001-US15718	20010516
WO 2001088197	A3	20031231		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-204509P P 20000516

AB The present invention provides methods and compns. for interaction trap assays for detecting protein-protein, protein-DNA, or protein-RNA interactions using prokaryotic or microbial eukaryotic hosts. The methods and compns. of the invention may also be used to identify agents which may agonize or antagonize a protein-protein, protein-DNA, or protein-RNA interaction. In certain embodiments, the interaction trap system of the invention is useful for screening libraries with greater than 107 members. In other embodiments, the interaction trap system of the invention is used in conjunction with flow cytometry. The invention further provides a means for simultaneously screening a target protein or nucleic acid sequence for the ability to interact with two or more test proteins or nucleic acids. In one form, the screening involves the use of a selectable marker allowing screening of large nos. of cells without the need to scan for a colorimetric marker. In a second form, screening of a colorimetric marker is by flow cytometry. Screening of a library of 108 members in Escherichia coli for C2H2 zinc finger variants is demonstrated.

L14 ANSWER 21 OF 30 MEDLINE on STN DUPLICATE 10
ACCESSION NUMBER: 2002121249 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11842428
TITLE: Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system.
AUTHOR: Joung J K
CORPORATE SOURCE: Department of Pathology, Division of Molecular Pathology and Research, Massachusetts General Hospital, Charlestown, Massachusetts 02129, USA.. jjoung@partners.org
CONTRACT NUMBER: 1 K08 DK02883-01 (NIDDK)
SOURCE: Journal of cellular biochemistry. Supplement, (2001) Vol.

Suppl 37, pp. 53-7. Ref: 12
Journal code: 8207539. ISSN: 0733-1959.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 22 Feb 2002
Last Updated on STN: 14 Feb 2003
Entered Medline: 29 Apr 2002

AB A bacterial two-hybrid system based on transcriptional activation in E. coli has recently been described. A variety of different protein-DNA and protein-protein interactions from bacteria, yeast, and humans have been studied using this bacterial-based system. The method, because it is based in bacteria, offers significant advantages relative to its yeast counterpart including the ability to analyze complex libraries > 10(8) in size, ease of use, and speed. The ability to easily and rapidly process very large libraries make this system a powerful tool for identifying, modifying, or optimizing protein-DNA and protein-protein interactions. Copyright 2002 Wiley-Liss, Inc.

L14 ANSWER 22 OF 30 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2002:168852 SCISEARCH
THE GENUINE ARTICLE: 520VN
TITLE: Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system
AUTHOR: Joung J K (Reprint)
CORPORATE SOURCE: Massachusetts Gen Hosp, Div Mol Pathol & Res, Dept Pathol, 149 13th St, 7th Floor, Charlestown, MA 02129 USA (Reprint); Massachusetts Gen Hosp, Div Mol Pathol & Res, Dept Pathol, Charlestown, MA 02129 USA
jjoung@partners.org
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF CELLULAR BIOCHEMISTRY, (2001) Vol. 84, Supp. [37], pp. 53-57.
ISSN: 0730-2312.
PUBLISHER: WILEY-LISS, DIV JOHN WILEY & SONS INC, 111 RIVER ST, HOBOKEN, NJ 07030 USA.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 12
ENTRY DATE: Entered STN: 12 Mar 2002
Last Updated on STN: 7 Dec 2006
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A bacterial two-hybrid system based on transcriptional activation in E. coli has recently been described. A variety of different protein-DNA and protein-protein interactions from bacteria, yeast, and humans have been studied using this bacterial-based system. The method, because it is based in bacteria, offers significant advantages relative to its yeast counterpart including the ability to analyze complex libraries >10(8) in size, ease of use, and speed. The ability to easily and rapidly process very large libraries make this system a powerful tool for identifying, modifying, or optimizing protein-DNA and protein-protein interactions. (C) 2002 Wiley-Liss, Inc.

L14 ANSWER 23 OF 30 MEDLINE on STN DUPLICATE 11
ACCESSION NUMBER: 2000319035 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10852947
TITLE: A bacterial two-hybrid selection system for studying protein-DNA and protein-protein interactions.

AUTHOR: Joung J K; Ramm E I; Pabo C O
CORPORATE SOURCE: Howard Hughes Medical Institute and Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02139, USA.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2000 Jun 20) Vol. 97, No. 13, pp. 7382-7.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 11 Aug 2000
Last Updated on STN: 11 Aug 2000
Entered Medline: 31 Jul 2000

AB We have developed a bacterial "two-hybrid" system that readily allows selection from libraries larger than 10(8) in size. Our bacterial system may be used to study either protein-DNA or protein-protein interactions, and it offers a number of potentially significant advantages over existing yeast-based one-hybrid and two-hybrid methods. We tested our system by selecting zinc finger variants (from a large randomized library) that bind tightly and specifically to desired DNA target sites. Our method allows sequence-specific zinc fingers to be isolated in a single selection step, and thus it should be more rapid than phage display strategies that typically require multiple enrichment/amplification cycles. Given the large library sizes our bacterial-based selection system can handle, this method should provide a powerful tool for identifying and optimizing protein-DNA and protein-protein interactions.

L14 ANSWER 24 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1999:450862 CAPLUS
DOCUMENT NUMBER: 131:83957
TITLE: Interaction trap assay and its reagents
INVENTOR(S): Dove, Simon; Joung, J. Keith; Hochschild, Ann
PATENT ASSIGNEE(S): President & Fellows of Harvard College, USA
SOURCE: U.S., 28 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 5925523	A	19990720	US 1997-920015		19970826
US 6200759	B1	20010313	US 1999-296204		19990421
PRIORITY APPLN. INFO.:			US 1996-24484P	P	19960823
			US 1997-918612	B2	19970822
			US 1997-920015	A1	19970826

AB The present invention makes available an interaction trap system which is derived using recombinantly engineered prokaryotic cells. An interaction trap or two-hybrid system designed for use in a prokaryotic, i.e. bacterial, host is described. The system is generally similar to those designed for use with yeast but using components derived solely from prokaryotes. In particular a system using fusion proteins of the λ cI repressor that bind an OR2 operator in a modified lacP/O promoter-operator region is described. The second component of the binding assay may be a fusion protein of the α or ω subunits of the bacterial RNA polymerase. Alternatively, the LexA repressor may be used in combination with the SOS box.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 25 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 12
ACCESSION NUMBER: 1998:151232 CAPLUS
DOCUMENT NUMBER: 128:201791
TITLE: An interaction trap assay system using the λ repressor for use in a bacterial host
INVENTOR(S): Dove, Simon; Joung, J. Keith; Hochschild, Ann
PATENT ASSIGNEE(S): President and Fellows of Harvard College, USA
SOURCE: PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 9807845	A1	19980226	WO 1997-US14860		19970822
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN					
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
AU 9741596	A	19980306	AU 1997-41596		19970822
US 6982082	B1	20060103	US 1997-922240		19970827
PRIORITY APPLN. INFO.:			US 1996-24484P	P	19960823
			WO 1997-US14860	W	19970822

AB An interaction trap or two-hybrid system designed for use in a prokaryotic, i.e. bacterial, host is described. The system is generally similar to those designed for use with yeast but using components derived solely from prokaryotes. In particular a system using fusion proteins of the λ cI repressor that bind an OR2 operator in a modified lacP/O promoter-operator region is described. The second component of the binding assay may be a fusion protein of the α or ω subunits of the bacterial RNA polymerase. Alternatively, the LexA repressor may be used in combination with the SOS box.
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 26 OF 30 MEDLINE on STN DUPLICATE 13
ACCESSION NUMBER: 97256540 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9121589
TITLE: Activation of prokaryotic transcription through arbitrary protein-protein contacts.
AUTHOR: Dove S L; Joung J K; Hochschild A
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA.
SOURCE: Nature, (1997 Apr 10) Vol. 386, No. 6625, pp. 627-30.
Journal code: 0410462. ISSN: 0028-0836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 6 May 1997
Last Updated on STN: 6 Feb 1998
Entered Medline: 22 Apr 1997

AB Many transcriptional activators in prokaryotes are known to bind near a promoter and contact RNA polymerase, but it is not clear whether a protein-protein contact between an activator and RNA polymerase is enough to activate gene transcription. Here we show that contact between a DNA-bound protein and a heterologous protein domain fused to RNA polymerase can elicit transcriptional activation; moreover, the strength of this engineered protein-protein interaction determines the amount of gene activation. Our results indicate that an arbitrary interaction between a DNA-bound protein and RNA polymerase can activate transcription. We also find that when the DNA-bound 'activator' makes contact with two different components of the polymerase, the effect of these two interactions on transcription is synergistic.

L14 ANSWER 27 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1997:634127 CAPLUS
DOCUMENT NUMBER: 127:315154
TITLE: Synergistic activation of transcription in E. coli
AUTHOR(S): Hochschild, A.; Joung, J. K.
CORPORATE SOURCE: Dep. Microbiology & Molecular Genetics, Harvard Medical School, Boston, MA, 02115, USA
SOURCE: Nucleic Acids and Molecular Biology (1997), 11(Mechanisms of Transcription), 101-114
CODEN: NAMBE8; ISSN: 0933-1891
PUBLISHER: Springer
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review with several refs. Transcriptional activation in prokaryotes can involve the action of a single DNA-bound regulator or the combined action of two or more regulators working synergistically. In this chapter, the authors review some recent examples of transcriptional activator synergy and discuss the underlying mechanisms. For the purposes of this discussion, the authors follow the convention generally observed in the field and define transcriptional activator synergy as follows: the action of two (or more) activators is defined as synergistic if the amount of transcription observed in the presence of both activators (or both binding sites) is greater than the sum of the amts. observed with each activator acting on its own.
REFERENCE COUNT: 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 28 OF 30 MEDLINE on STN DUPLICATE 14
ACCESSION NUMBER: 96101597 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7498794
TITLE: Genetic strategy for analyzing specificity of dimer formation: Escherichia coli cyclic AMP receptor protein mutant altered in its dimerization specificity.
AUTHOR: Joung J K; Chung E H; King G; Yu C; Hirsh A S; Hochschild A
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA.
SOURCE: Genes & development, (1995 Dec 1) Vol. 9, No. 23, pp. 2986-96.
Journal code: 8711660. ISSN: 0890-9369.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199601
ENTRY DATE: Entered STN: 17 Feb 1996
Last Updated on STN: 17 Feb 1996
Entered Medline: 18 Jan 1996
AB Many transcriptional regulators function in homo- or heterodimeric

combinations. The same protein can carry out distinct regulatory functions depending on the partner with which it associates. Here, we describe a mutant of the Escherichia coli cAMP receptor protein (CRP) that has an altered dimerization specificity; that is, mutant/mutant homodimers form preferentially over wild-type/mutant heterodimers. CRP dimerization involves the formation of a parallel coiled-coil structure, and our CRP mutant bears an amino acid substitution affecting the first "d" position residue within the alpha-helix that mediates CRP dimerization. The genetic strategy we used to isolate this CRP altered dimerization specificity (ADS) mutant is generalizable and could be utilized to isolate ADS mutants of other dimeric transcriptional regulators.

L14 ANSWER 29 OF 30 MEDLINE on STN DUPLICATE 15
ACCESSION NUMBER: 94377980 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8091212
TITLE: Synergistic activation of transcription by bacteriophage lambda cI protein and E. coli cAMP receptor protein.
AUTHOR: Joung J K; Koepp D M; Hochschild A
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, MA 02115.
CONTRACT NUMBER: GM44025 (NIGMS)
SOURCE: Science, (1994 Sep 23) Vol. 265, No. 5180, pp. 1863-6.
Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199410
ENTRY DATE: Entered STN: 31 Oct 1994
Last Updated on STN: 6 Feb 1998
Entered Medline: 19 Oct 1994

AB Two heterologous prokaryotic activators, the bacteriophage lambda cI protein (lambda cI) and the Escherichia coli cyclic AMP receptor protein (CRP), were shown to activate transcription synergistically from an artificial promoter bearing binding sites for both proteins. The synergy depends on a functional activation (positive control) surface on each activator. These results imply that both proteins interact directly with RNA polymerase and thus suggest a precise mechanism for transcriptional synergy: the interaction of two activators with two distinct surfaces of RNA polymerase.

L14 ANSWER 30 OF 30 MEDLINE on STN DUPLICATE 16
ACCESSION NUMBER: 93219429 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7681995
TITLE: Synergistic activation of transcription by Escherichia coli cAMP receptor protein.
AUTHOR: Joung J K; Le L U; Hochschild A
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, MA 02115.
CONTRACT NUMBER: GM44025 (NIGMS)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1993 Apr 1) Vol. 90, No. 7, pp. 3083-7.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199305
ENTRY DATE: Entered STN: 21 May 1993
Last Updated on STN: 6 Feb 1998
Entered Medline: 4 May 1993

AB Activation of gene expression in eukaryotes generally involves the action of multiple transcription factors that function synergistically when bound near a particular target gene. Such effects have been suggested to occur because multiple activators can interact simultaneously with one or more components of the basal transcription machinery. In prokaryotes, examples of synergistic effects on transcription are much more limited and can often be explained by cooperative DNA binding. Here we show that the Escherichia coli cAMP receptor protein (CRP) functions synergistically to activate transcription from a derivative of the lac promoter that bears a second CRP-binding site upstream of the natural binding site. We present evidence indicating that cooperative DNA binding of two CRP dimers does not account for the magnitude of the observed cooperative activation. We suggest, instead, that the two dimers stimulate transcription directly by contacting two distinct surfaces of RNA polymerase simultaneously. Thus, synergistic activation by CRP may provide a relatively simple model for examining the molecular basis of such effects in higher organisms.

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FILE 'MEDLINE, BIOSIS, CAPLUS, SCISEARCH, EMBASE, WPIDS' ENTERED AT 14:35:32 ON 02 JAN 2007

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L1            0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN) AND (BIND OR INTERAC
L2            0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN) AND (BIND OR INTERAC
L3            0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN) AND (BIND OR INTERAC
L4            0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN) AND (BIND OR INTERAC
L5            0 IDENTIF? (S) (DNA ADJ BINDING ADJ PROTEIN)
L6            0 IDENTIF (S) (DNA (W) BINDING (W)  PROTEIN) AND (BIND OR INTERAC
L7            0 IDENTIF (S) (DNA (A) BINDING (A)  PROTEIN) AND (BIND OR INTERAC
L8            0 IDENTIF (S) (DNA (A) BINDING (A)  PROTEIN) AND REPORTER AND FUS
L9           25 IDENTIF? (S) (DNA (A) BINDING (A)  PROTEIN) AND REPORTER AND FU
L10          20 DUP REM L9 (5 DUPLICATES REMOVED)
                E JOUNG J?/AU
                E JOUNG J K?/AU
L11          77 E2 OR E4
L12          57 DNA AND L11
L13          25 DUP REM L12 (32 DUPLICATES REMOVED)
L14          30 DUP REM L11 (47 DUPLICATES REMOVED)
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